

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Reed, Steven G.
Skeiky, Yasir A.W.
Dillon, Davin C.
Campos-Neto, Antonio
Houghton, Raymond
Vedvick, Thomas S.
Twardzik, Daniel R.
Lodes, Michael J.
Hendrickson, Ronald
- (ii) TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS
- (iii) NUMBER OF SEQUENCES: 355
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: SEED and BERRY LLP
(B) STREET: 6300 Columbia Center, 701 Fifth Avenue
(C) CITY: Seattle
(D) STATE: Washington
(E) COUNTRY: USA
(F) ZIP: 98104-7092
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 05-MAY-1998
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Maki, David J.
(B) REGISTRATION NUMBER: 31,392
(C) REFERENCE/DOCKET NUMBER: 210121.411C9
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (206) 622-4900
(B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 766 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

20050420 1008443 02502

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGAGGCACCG | GTAGTTTGAA | CCAAACGCAC | AATCGACGGG | CAAACGAACG | GAAGAACACA | 60 |
| ACCATGAAGA | TGGTGAAATC | GATCGCCGCA | GGTCTGACCG | CCGCGGCTGC | AATCGGCGCC | 120 |
| GCTGCGGCCG | GTGTGACTTC | GATCATGGCT | GGCGGCCCGG | TCGTATACCA | GATGCAGCCG | 180 |
| GTCGTCTTCG | GCGCGCCACT | GCCGTTGGAC | CCGGCATCCG | CCCCTGACGT | CCCGACCGCC | 240 |
| GCCCAGTTGA | CCAGCCTGCT | CAACAGCCTC | GCCGATCCCA | ACGTGTCGTT | TGCGAACAAG | 300 |
| GGCAGTCTGG | TCGAGGGCGG | CATCGGGGGC | ACCGAGGCGC | GCATCGCCGA | CCACAAGCTG | 360 |
| AAGAAGGCCG | CCGAGCACGG | GGATCTGCCG | CTGTCGTTCA | GCGTGACGAA | CATCCAGCCG | 420 |
| GCGGCCGCCG | GTTCCGCCAC | CGCCGACGTT | TCCGTCTCGG | GTCCGAAGCT | CTCGTCGCCG | 480 |
| GTCACGCAGA | ACGTCACGTT | CGTGAATCAA | GGCGGCTGGA | TGCTGTCACG | CGCATCGGCG | 540 |
| ATGGAGTTGC | TGCAGGCCGC | AGGGNAACTG | ATTGGCGGGC | CGGNTTCAGC | CCGCTGTTC | 600 |
| GCTACGCCGC | CCGCTGGTG | ACGCGTCCAT | GTCGAACACT | CGCGCGTGTA | GCACGGTGCG | 660 |
| GTNTGCGCAG | GGNCGCACGC | ACCGCCCGGT | GCAAGCCGTC | CTCGAGATAG | GTGGTGNTCT | 720 |
| GNCACCAGNG | ANCACCCCN | NNTCGNCNNT | TCTCGNTGNT | GNATGA | | 766 |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ATGCATCACC | ATCACCATCA | CGATGAAGTC | ACGGTAGAGA | CGACCTCCGT | CTTCCGCGCA | 60 |
| GACTTCCTCA | GCGAGCTGGA | CGCTCCTGCG | CAAGCGGGTA | CGGAGAGCGC | GGTCTCCGGG | 120 |
| GTGGAAGGGC | TCCCGCCGGG | CTCGGCGTTG | CTGGTAGTCA | AACGAGGCCC | CAACGCCGGG | 180 |
| TCCCGGTTCC | TACTCGACCA | AGCCATCACG | TCGGCTGGTC | GGCATCCCGA | CAGCGACATA | 240 |
| TTTCTCGACG | ACGTGACCGT | GAGCCGTCGC | CATGCTGAAT | TCCGGTTGGA | AAACAACGAA | 300 |
| TTCAATGTTC | TCGATGTCGG | GAGTCTCAAC | GGCACCTACG | TCAACCGCGA | GCCCGTGGAT | 360 |
| TCGGCGGTGC | TGGCGAACGG | CGACGAGGTC | CAGATCGGCA | AGCTCCGGTT | GGTGTTCTTG | 420 |
| ACCGGACCCA | AGCAAGGCGA | GGATGACGGG | AGTACCGGGG | GCCCGTGAGC | GCACCCGATA | 480 |
| GCCCCGCGCT | GGCCGGGATG | TCGATCGGGG | CGGTCTCCG | ACCTGCTACG | ACCGGATTTT | 540 |
| CCCTGATGTC | CACCATCTCC | AAGATTCGAT | TCCTGGGAGG | CTTGAGGGTC | NGGGTGACCC | 600 |
| CCCCGCGGGC | CTCATTCNGG | GGTNTCGGCN | GGTTTCACCC | CNTACCNACT | GCCNCCCGGN | 660 |
| TTGCNAATTC | NTTCTTCNCT | GCCCNAAAG | GGACCNTTAN | CTTGCCGCTN | GAAANGGTNA | 720 |
| TCCNGGGCCC | NTCCTNGAAN | CCCCNTCCCC | CT | | | 752 |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CATATGCATC | ACCATCACCA | TCACACTTCT | AACCGCCCAG | CGCGTCGGGG | GCGTCGAGCA | 60 |
| CCACGCGACA | CCGGGCCCCG | TCGATCTGCT | AGCTTGAGTC | TGGTCAGGCA | TCGTCTGCAG | 120 |
| CAGCGCGATG | CCCTATGTTT | GTCGTGCACT | CAGATATCGC | GGCAATCCAA | TCTCCGCGCT | 180 |

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| GCGGCCGGCG | GTGCTGCAAA | CTACTCCCGG | AGGAATTTTCG | ACGTGCGCAT | CAAGATCTTC | 240 |
| ATGCTGGTCA | CGGCTGTCGT | TTTGCTCTGT | TGTTTCGGGTG | TGGCCACGGC | CGCGCCCAAG | 300 |
| ACCTACTGCG | AGGAGTTGAA | AGGCACCGAT | ACCGGCCAGG | CGTGCCAGAT | TCAAATGTCC | 360 |
| GACCCGGCCT | ACAACATCAA | CATCAGCCTG | CCCAGTTACT | ACCCCGACCA | GAAGTCGCTG | 420 |
| GAAAATTACA | TCGCCCAGAC | GCGCGACAAG | TTCCTCAGCG | CGGCCACATC | GTCCACTCCA | 480 |
| CGCGAAGCCC | CCTACGAATT | GAATATCACC | TCGGCCACAT | ACCAGTCCGC | GATACCGCCG | 540 |
| CGTGGTACGC | AGGCCGTGGT | GCTCAMGGTC | TACCACAACG | CCGGCGGCAC | GCACCCAACG | 600 |
| ACCACGTACA | AGGCCTTCGA | TTGGGACCAG | GCCTATCGCA | AGCCAATCAC | CTATGACACG | 660 |
| CTGTGGCAGG | CTGACACCGA | TCCGCTGCCA | GTCTCTTCC | CCATTGTTGC | AAGGTGAACT | 720 |
| GAGCAACGCA | GACCGGGACA | ACWGGTATCG | ATAGCCGCCN | AATGCCGGCT | TGGAACCCNG | 780 |
| TGAAATTATC | ACAACCTTCG | AGTCACNAAA | NAA | | | 813 |

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | | | | |
|-------------|-------------|------------|------------|-------------|------------|-----|
| CGGTATGAAC | ACGGCCGCGT | CCGATAACTT | CCAGCTGTCC | CAGGGTGGGC | AGGGATTTCG | 60 |
| CATTCCGATC | GGGCAGGCGA | TGGCGATCGC | GGGCCAGATC | CGATCGGGTG | GGGGGTCACC | 120 |
| CACCGTTTCAT | ATCGGGCCTA | CCGCCTTCCT | CGGCTTGGGT | GTGTGTCGACA | ACAACGGCAA | 180 |
| CGGCGCACGA | GTCCAACGCG | TGGTCGGGAG | CGCTCCGGCG | GCAAGTCTCG | GCATCTCCAC | 240 |
| CGGCGACGTG | ATCACC GCGG | TCGACGGCGC | TCCGATCAAC | TCGGCCACCG | CGATGGCGGA | 300 |
| CGCGCTTAAC | GGGCATCATC | CCGGTGACGT | CATCTCGGTG | AACTGGCAAA | CCAAGTCGGG | 360 |
| CGGCACGCGT | ACAGGGAACG | TGACATTGGC | CGAGGGACCC | CCGGCCTGAT | TTCGTCGYGG | 420 |
| ATACCACCCG | CCGGCCGGCC | AATTGGA | | | | 447 |

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

| | | | | | | |
|------------|-------------|------------|------------|------------|-------------|-----|
| GTCCCACTGC | GGTCGCCGAG | TATGTCGCC | AGCAAATGTC | TGGCAGCCGC | CCAACGGAAT | 60 |
| CCGGTGATCC | GACGTCGCAG | GTGTGCGAAC | CCGCCGCCGC | GGAAGTATCG | GTCCATGCCT | 120 |
| AGCCCGGCGA | CGGCGAGCGC | CGGAATGGCG | CGAGTGAGGA | GGCGGGCAAT | TTGGCGGGGC | 180 |
| CCGGCGACGG | NGAGCGCCGG | AATGGCGCGA | GTGAGGAGGT | GGNCAGTCAT | GCCCAGNGTG | 240 |
| ATCCAATCAA | CCTGNATTCTG | GNCTGNNGGN | CCATTGACA | ATCGAGGTAG | TGAGCGCAAA | 300 |
| TGAATGATGG | AAAACGGGNG | GNGACGTCCG | NTGTTCTGGT | GGTGNTAGGT | GNCTGNCTGG | 360 |
| NGTNGNGGNT | ATCAGGATGT | TCTTCGNCGA | AANCTGATGN | CGAGGAACAG | GGTGTNCCCCG | 420 |
| NNANNCCNAN | GGNGTCCNAN | CCCNNTTCC | TCGNCGANAT | CANANAGNCG | NTTGATGNGA | 480 |
| NAAAAGGGTG | GANCAGNNNN | AANTNGNGGN | CCNAANAANC | NNNANNGNNG | NNAGNTNGNT | 540 |
| NNNTNTTNNC | ANNNNNNTTG | NGNNGNNGCN | NNNCAANCNN | NTNNNNGNAA | NNGGNTTNTT | 600 |
| NAAT | | | | | | 604 |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| TTGCANGTCG | AACCACCTCA | CTAAAGGGAA | CAAAAGCTNG | AGCTCCACCG | CGGTGGCGGC | 60 |
| CGCTCTAGAA | CTAGTGKATM | YYYCKGGCTG | CAGSAATYCG | GYACGAGCAT | TAGGACAGTC | 120 |
| TAACGGTCCT | GTTACGGTGA | TCGAATGACC | GACGACATCC | TGCTGATCGA | CACCGACGAA | 180 |
| CGGGTGCGAA | CCCTCACCT | CAACCGGCCG | CAGTCCCGYA | ACGCGCTCTC | GGCGGCGCTA | 240 |
| CGGGATCGGT | TTTTCGCGGY | GTTGGYCGAC | GCCGAGGYCG | ACGACGACAT | CGACGTCGTC | 300 |
| ATCCTCACCG | GYGCCGATCC | GGTGTTCTGC | GCCGACTGG | ACCTCAAGGT | AGCTGGCCGG | 360 |
| GCAGACCGCG | CTGCCGGACA | TCTCACCGCG | GTGGGCGGCC | ATGACCAAGC | CGGTGATCGG | 420 |
| CGCGATCAAC | GGCGCCGCGG | TCACCGGCGG | GCTCGAACTG | GCGCTGTACT | GCGACATCCT | 480 |
| GATCGCCTCC | GAGCACGCCC | GCTTCGNCGA | CACCCACGCC | CGGGTGGGGC | TGCTGCCCCAC | 540 |
| CTGGGGACTC | AGTGTGTGCT | TGCCGCAAAA | GGTCGGCATC | GGNCTGGGCC | GGTGGATGAG | 600 |
| CCTGACCGGC | GACTACCTGT | CCGTGACCGA | CGC | | | 633 |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | | | | | | |
|------------|------------|-------------|-------------|------------|-------------|------|
| CGACGACGAC | GGCGCCGGAG | AGCGGGCGCG | AACGGCGATC | GACGCGGCCC | TGGCCAGAGT | 60 |
| CGGCACCACC | CAGGAGGGAG | TCGAATCATG | AAATTTGTCA | ACCATATTGA | GCCCGTCGCG | 120 |
| CCCCGCCGAG | CCGGCGGCGC | GGTCGCCGAG | GTCTATGCCG | AGGCCCGCCG | CGAGTTCGGC | 180 |
| CGGCTGCCCC | AGCCGCTCGC | CATGCTGTCC | CCGGACGAGG | GACTGCTCAC | CGCCGGCTGG | 240 |
| GCGACGTTGC | GCGAGACACT | GCTGGTGGGC | CAGGTGCCGC | GTGGCCGCAA | GGAAGCCGTC | 300 |
| GCCGCCGCCG | TCGCGGCCAG | CCTGCGCTGC | CCCTGGTGCG | TCGACGCACA | CACCACCATG | 360 |
| CTGTACCGCG | CAGGCCAAAC | CGACACCGCC | GCGGCGATCT | TGGCCGGCAC | AGCACCTGCC | 420 |
| GCCGGTGACC | CGAACCAGCC | GTATGTGGCG | TGGGCGGCAG | GAACCGGGAC | ACCGGCGGGA | 480 |
| CCGCCGGCAC | CGTTCGGCCC | GGATGTCGCC | GCCGAATACC | TGGGCACCGC | GGTGCAATTC | 540 |
| CACTTCATCG | CACGCCTGGT | CCTGGTGCTG | CTGGACGAAA | CCTTCCTGCC | GGGGGGCCCG | 600 |
| CGCGCCCAAC | AGCTCATGCG | CCGCGCCGGT | GGACTGGTGT | TCGCCCAGAA | GGTGCGCGCG | 660 |
| GAGCATCGGC | CGGGCCGCTC | CACCCGCCGG | CTCGAGCCGC | GAACGCTGCC | CGACGATCTG | 720 |
| GCATGGGCAA | CACCGTCCGA | GCCCATAGCA | ACCGCGTTTCG | CCGCGCTCAG | CCACCACCTG | 780 |
| GACACCGCGC | CGCACCTGCC | GCCACCGACT | CGTCAGGTGG | TCAGGCGGGT | CGTGGGGTTCG | 840 |
| TGGCACGGCG | AGCCAATGCC | GATGAGCAGT | CGCTGGACGA | ACGAGCACAC | CGCCGAGCTG | 900 |
| CCCGCCGACC | TGCACGCGCC | CACCCGTCTT | GCCCTGCTGA | CCGGCCTGGC | CCCGCATCAG | 960 |
| GTGACCGACG | ACGACGTCGC | CGCGGCCCGA | TCCCTGCTCG | ACACCGATGC | GGCGCTGGTT | 1020 |
| GGCGCCCTGG | CCTGGGCCGC | CTTCACCGCC | GCGCGGCGCA | TCGGCACCTG | GATCGGCGCC | 1080 |
| GCCGCCGAGG | GCCAGGTGTC | GCGGCAAAAC | CCGACTGGGT | GAGTGTGCGC | GCCCTGTCCG | 1140 |
| TAGGGTGTC | TCGCTGGCCC | GAGGGATCTC | GCGGCGGCGA | ACGGAGGTGG | CGACACAGGT | 1200 |
| GGAAGCTGCG | CCCAGTGGCT | TGCGCCCCAA | CGCCGTCGTG | GGCGTTCCGT | TGGCCGCACT | 1260 |
| GGCCGATCAG | GTCGGCGCCG | GCCCTTGCC | GAAGGTCCAG | CTCAACGTGC | CGTCACCGAA | 1320 |
| GGACCGGACG | GTCACCGGGG | GTCACCCCTGC | GCGCCCAAGG | AA | | 1362 |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

| | | | | | | |
|------------|------------|-------------|-------------|------------|------------|------|
| GCGACGACCC | CGATATGCCG | GGCACCGTAG | CGAAAGCCGT | CGCCGACGCA | CTCGGGCGCG | 60 |
| GTATCGCTCC | CGTTGAGGAC | ATTCAGGACT | GCGTGAGGAC | CCGGCTGGGG | GAAGCCGGTC | 120 |
| TGGATGACGT | GGCCCGTGTT | TACATCATCT | ACCGGCAGCG | GCGCGCCGAG | CTGCGGACGG | 180 |
| CTAAGGCCTT | GCTCGGCGTG | CGGGACGAGT | TAAAGCTGAG | CTTGGCGGCC | GTGACGGTAC | 240 |
| TGCGCGAGCG | CTATCTGCTG | CACGACGAGC | AGGGCCGGCC | GGCCGAGTCG | ACCGGCGAGC | 300 |
| TGATGGACCG | ATCGGCGCGC | TGTGTCGCGG | CGGCCGAGGA | CCAGTATGAG | CCGGGCTCGT | 360 |
| CGAGGCGGTG | GGCCGAGCGG | TTCGCCACGC | TATTACGCAA | CCTGGAATTC | CTGCCGAATT | 420 |
| CGCCACGTT | GATGAAGTCT | GGCACCGACC | TGGGACTGCT | CGCCGGCTGT | TTTGTTCTGC | 480 |
| CGATTGAGGA | TTGCTGCAA | TGCATCTTTG | CGACGCTGGG | ACAGGCCGCC | GAGCTGCAGC | 540 |
| GGGCTGGAGG | CGGCACCGGA | TATGCGTTCA | GCCACCTGCG | ACCCGCCGGG | GATCGGGTGG | 600 |
| CCTCCACGGG | CGGCACGGCC | AGCGGACCGG | TGTCGTTTCT | ACGGCTGTAT | GACAGTGCCG | 660 |
| CGGGTGTGGT | CTCCATGGGC | GGTCGCCGGC | GTGGCGCCTG | TATGGCTGTG | CTTGATGTGT | 720 |
| CGCACCCGGA | TATCTGTGAT | TTCGTCACCG | CCAAGGCCGA | ATCCCCCAGC | GAGCTCCCGC | 780 |
| ATTTCAACCT | ATCGGTTGGT | GTGACCGACG | CGTTCCTGCG | GGCCGTCGAA | CGCAACGGCC | 840 |
| TACACCGGCT | GGTCAATCCG | CGAACC GGCA | AGATCGTCGC | GCGGATGCCC | GCCGCCGAGC | 900 |
| TGTTGACGCG | CATCTGCAAA | GCCGCGCAGC | CCGGTGCGCA | TCCCGGGCTG | GTGTTTCTCG | 960 |
| ACACGATCAA | TAGGGCAAAC | CCGGTGCCGG | GGAGAGGCCG | CATCGAGGCG | ACCAACCCGT | 1020 |
| GCGGGGAGGT | CCCACTGCTG | CCTTACGAGT | CATGTAATCT | CGGCTCGATC | AACCTCGCCC | 1080 |
| GGATGCTCGC | CGACGGTCGC | GTGACTGGG | ACCGGCTCGA | GGAGGTGCGC | GGTGTGGCGG | 1140 |
| TGCGGTTTCT | TGATGACGTC | ATCGATGTCA | GCCGCTACCC | CTTCCCCGAA | CTGGGTGAGG | 1200 |
| CGGCCCCGCG | CACCCGCAAG | ATCGGGCTGG | GAGTCATGGG | TTTGGCGGAA | CTGCTTGCCG | 1260 |
| CACTGGGTAT | TCCGTACGAC | AGTGAAGAAG | CCGTGCGGTT | AGCCACCCGG | CTCATGCGTC | 1320 |
| GCATACAGCA | GGCGGCGCAC | ACGGCATCGC | GGAGGCTGGC | CGAAGAGCGG | GGCGCATTC | 1380 |
| CGGCGTTTAC | CGATAGCCGG | TTGCGCGGGT | CGGGCCCCGAG | GCGCAACGCA | CAGGTCACCT | 1440 |
| CCGTCGCTCC | GACGGGCA | | | | | 1458 |

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACGGTGTAAT | CGTGCTGGAT | CTGGAACCGC | GTGGCCCCGT | ACCTACCGAG | ATCTACTGGC | 60 |
| GGCGCAGGGG | GCTGGCCCTG | GGCATCGCGG | TCGTGCTAGT | CGGGATCGCG | GTGGCCATCG | 120 |
| TCATCGCCTT | CGTCGACAGC | AGCGCCGGTG | CCAAACCGGT | CAGCGCCGAC | AAGCCGGCCT | 180 |
| CCGCCCAGAG | CCATCCGGGC | TCGCCGGCAC | CCCAAGCACC | CCAGCCGGCC | GGGCAAACCG | 240 |
| AAGGTAACGC | CGCCGCGGCC | CCGCCGAGG | GCCAAAACCC | CGAGACACCC | ACGCCACCG | 300 |
| CCGCGGTGCA | GCCGCCGCCG | GTGCTCAAG | AAGGGGACGA | TTGCCCCGAT | TCGACGCTGG | 360 |
| CCGTCAAAGG | TTTGACCAAC | GCGCCGAGT | ACTACGTCGG | CGACCAGCCG | AAGTTCACCA | 420 |
| TGGTGGTCAC | CAACATCGGC | CTGGTGTCCT | GTAACGCAGA | CGTTGGGGCC | GCGGTGTGG | 480 |
| CCGCCTACGT | TTACTCGCTG | GACAACAAGC | GGTTGTGGTC | CAACCTGGAC | TGCGCGCCCT | 540 |
| CGAATGAGAC | GCTGGTCAAG | ACGTTTTCCC | CCGGTGAGCA | GGTAACGACC | GCGGTGACCT | 600 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GGACCGGGAT | GGGATCGGCG | CCGCGCTGCC | CATTGCCGCG | GCCGGCGATC | GGGCCGGGCA | 660 |
| CCTACAATCT | CGTGGTACAA | CTGGGCAATC | TGCGCTCGCT | GCCGGTTCCG | TTCATCCTGA | 720 |
| ATCAGCCGCC | GCCGCCGCCC | GGGCCGGTAC | CCGCTCCGGG | TCCAGCGCAG | GCGCCTCCGC | 780 |
| CGGAGTCTCC | CGCGCAAGGC | GGATAATTAT | TGATCGCTGA | TGGTCGATTG | CGCCAGCTGT | 840 |
| GACAACCCCT | CGCCTCGTGC | CG | | | | 862 |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTGATCAGCA | CCGGCAAGGC | GTCACATGCC | TCCCTGGGTG | TGCAGGTGAC | CAATGACAAA | 60 |
| GACACCCCGG | GCGCCAAGAT | CGTCGAAGTA | GTGGCCGGTG | GTGCTGCCGC | GAACGCTGGA | 120 |
| GTGCCGAAGG | GCGTCGTTGT | CACCAAGGTC | GACGACCGCC | CGATCAACAG | CGCGGACGCG | 180 |
| TTGGTTGCCG | CCGTGCGGTC | CAAAGCGCCG | GGCGCCACGG | TGGCGCTAAC | CTTTCAGGAT | 240 |
| CCCTCGGGCG | GTAGCCGCAC | AGTGCAAGTC | ACCCTCGGCA | AGGCGGAGCA | GTGATGAAGG | 300 |
| TCGCCGCGCA | GTGTTCAAAG | CTCGGATATA | CGGTGGCACC | CATGGAACAG | CGTGCGGAGT | 360 |
| TGGTGGTTGG | CCGGGCACTT | GTCGTCGTCG | TTGACGATCG | CACGGCGCAC | GGCGATGAAG | 420 |
| ACCACAGCGG | GCCGCTTGTC | ACCGAGCTGC | TCACCGAGGC | CGGGTTTGTT | GTCGACGGCG | 480 |
| TGGTGGCGGT | GTCGGCCGAC | GAGGTCGAGA | TCCGAAATGC | GCTGAACACA | GCGGTGATCG | 540 |
| GCGGGGTGGA | CCTGGTGGTG | TCGGTCGGCG | GGACCGNGT | GACGNCTCGC | GATGTCACCC | 600 |
| CGGAAGCCAC | CCGNGACATT | CT | | | | 622 |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|------|
| GGCGCAGCGG | TAAGCCTGTT | GGCCGCCGCG | ACACTGGTGT | TGACAGCATG | CGGCGGTGGC | 60 |
| ACCAACAGCT | CGTCGTCAGG | CGCAGGCGGA | ACGCTGGGGT | CGGTGCACTG | CGGCGGCAAG | 120 |
| AAGGAGCTCC | ACTCCAGCGG | CTCGACCGCA | CAAGAAAATG | CCATGGAGCA | GTTTCGTCTAT | 180 |
| GCCTACGTGC | GATCGTGCCC | GGGCTACACG | TTGGACTACA | ACGCCAACGG | GTCCGGTGCC | 240 |
| GGGGTGACCC | AGTTTCTCAA | CAACGAAACC | GATTTGCGCG | GCTCGGATGT | CCC GTTGAAT | 300 |
| CCGTCGACCG | GTCAACCTGA | CCGGTCGGCG | GAGCGGTGCG | GTTCCCCGGC | ATGGGACCTG | 360 |
| CCGACGGTGT | TCGGCCCGAT | CGCGATCACC | TACAATATCA | AGGGCGTGAG | CACGCTGAAT | 420 |
| CTTGACGGAC | CCACTACCGC | CAAGATTTTC | AACGGCACCA | TCACCGTGTG | GAATGATCCA | 480 |
| CAGATCCAAG | CCCTCAACTC | CGGCACCGAC | CTGCCGCCAA | CACCGATTAG | CGTTATCTTC | 540 |
| CGCAGCGACA | AGTCCGGTAC | GTCGGACAAC | TTCCAGAAAT | ACCTCGACGG | TGTATCCAAC | 600 |
| GGGGCGTGCG | GCAAAGGCGC | CAGCGAAACG | TTCAGCGGGG | GCGTCGGCGT | CGGCGCCAGC | 660 |
| GGGAACAACG | GAACGTCGGC | CCTACTGCAG | ACGACCGACG | GGTCGATCAC | CTACAACGAG | 720 |
| TGGTCGTTTG | CGGTGGGTAA | GCAGTTGAAC | ATGGCCCAGA | TCATCACGTC | GGCGGGTCCG | 780 |
| GATCCAAGTG | CGATCACCAC | CGAGTCGGTC | GGTAAGACAA | TCGCCGGGGC | CAAGATCATG | 840 |
| GGACAAGGCA | ACGACCTGGT | ATTGGACACG | TCGTCGTTCT | ACAGACCCAC | CCAGCCTGGC | 900 |
| TCTTACCCGA | TCGTGTGGC | GACCTATGAG | ATCGTCTGCT | CGAAATACCC | GGATGCGACG | 960 |
| ACCGGTACTG | CGGTAAGGGC | GTTTATGCAA | GCCGCGATTG | GTCCAGGCCA | AGAAGGCCTG | 1020 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| GACCAATACG | GCTCCATTCC | GTTGCCCAAA | TCGTTCCAAG | CAAAATTGGC | GGCCGCGGTG | 1080 |
| AATGCTATTT | CTTGACCTAG | TGAAGGGAAT | TCGACGGTGA | GCGATGCCGT | TCCGCAGGTA | 1140 |
| GGGTCGCAAT | TTGGGCCGTA | TCAGCTATTG | CGGCTGCTGG | GCCGAGGCGG | GATGGGCGAG | 1200 |

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

| | | | | | | |
|-------------|------------|-------------|------------|------------|-------------|------|
| GCAAGCAGCT | GCAGGTCGTG | CTGTTGACG | AACTGGGCAT | GCCGAAGACC | AAACGCACCA | 60 |
| AGACCGGCTA | CACCACGGAT | GCCGACGCGC | TGCAGTCGTT | GTTCGACAAG | ACCGGGCATC | 120 |
| CGTTTCTGCA | ACATCTGCTC | GCCCACCGCG | ACGTCAACCG | GCTCAAGGTC | ACCGTCGACG | 180 |
| GGTTGCTCCA | AGCGGTGGCC | GCCGACGGCC | GCATCCACAC | CACGTTCAAC | CAGACGATCG | 240 |
| CCGCGACCGG | CCGGCTCTCC | TCGACCGAAC | CCAACCTGCA | GAACATCCCG | ATCCGCACCG | 300 |
| ACGCGGGCCG | GCGGATCCGG | GACGCGTTCG | TGGTCGGGGA | CGGTTACGCC | GAGTTGATGA | 360 |
| CGGCCGACTA | CAGCCAGATC | GAGATGCGGA | TCATGGGGCA | CCTGTCCGGG | GACGAGGGCC | 420 |
| TCATCGAGGC | GTTCAACACC | GGGGAGGACC | TGTATTCGTT | CGTCGCGTCC | CGGGTGTTTCG | 480 |
| GTGTGCCCCAT | CGACGAGGTC | ACCGGCGAGT | TGCGGCGCCG | GGTCAAGGCG | ATGTCTTACG | 540 |
| GGCTGGTTTA | CGGGTTGAGC | GCCTACGGCC | TGTCGCAGCA | GTTGAAAATC | TCCACCGAGG | 600 |
| AAGCCAACGA | GCAGATGGAC | CGGTATTTTCG | CCCGATTTCG | CGGGGTGCGC | GACTACCTGC | 660 |
| GCGCCGTAGT | CGAGCGGGCC | CGCAAGGACG | GCTACACCTC | GACGGTGCTG | GGCCGTCGCC | 720 |
| GCTACCTGCC | CGAGCTGGAC | AGCAGCAACC | GTCAAGTGCG | GGAGGCCGCC | GAGCGGGCGG | 780 |
| CGCTGAACGC | GCCGATCCAG | GGCAGCGCGG | CCGACATCAT | CAAGGTGGCC | ATGATCCAGG | 840 |
| TCGACAAGGC | GCTCAACGAG | GCACAGCTGG | CGTCGCGCAT | GCTGCTGCAG | GTCCACGACG | 900 |
| AGCTGCTGTT | CGAAATCGCC | CCCGGTGAAC | GCGAGCGGGT | CGAGGCCCTG | GTGCGCGACA | 960 |
| AGATGGGCGG | CGCTTACCCG | CTCGACGTCC | CGCTGGAGGT | GTCGGTGGGC | TACGGCCGCA | 1020 |
| GCTGGGACGC | GGCGGCGCAC | TGAGTGCCGA | GCGTGATCT | GGGGCGGGAA | TTCGGCGATT | 1080 |
| TTTCCGCCCT | GAGTTCACGC | TCGGCGCAAT | CGGGACCGAG | TTTGTCCAGC | GTGTACCCGT | 1140 |
| CGAGTAGCCT | CGTCA | | | | | 1155 |

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

| | | | | | | |
|------------|-------------|------------|------------|------------|-------------|-----|
| GAGCGCCGTC | TGGTGTTTGA | ACGGTTTTAC | CGGTCGGCAT | CGGCACGGGC | GTTGCCGGGT | 60 |
| TCGGGCCTCG | GTTTGGCGAT | CGTCAAACAG | GTGGTGCTCA | ACCACGGCGG | ATTGCTGCGC | 120 |
| ATCGAAGACA | CCGACCCAGG | CGGCCAGCCC | CCTGGAACGT | CGATTTACGT | GCTGCTCCCC | 180 |
| GGCCGTCCGA | TGCCGATTCC | GCAGCTTCCC | GGTGCGACGG | CTGGCGCTCG | GAGCACGGAC | 240 |
| ATCGAGAACT | CTCGGGGTTT | GGCGAACGTT | ATCTCAGTGG | AATCTCAGTC | CACGCGCGCA | 300 |
| ACCTAGTTGT | GCAGTTACTG | TTGAAAGCCA | CACCCATGCC | AGTCCACGCA | TGGCCAAAGTT | 360 |
| GGCCCAGTA | GTGGGCCCTAG | TACAGGAAGA | GCAACCTAGC | GACATGACGA | ATCACCACG | 420 |
| GTATTCGCCA | CCGCCGAGC | AGCCGGGAAC | CCCAGTTAT | GCTCAGGGGC | AGCAGCAAAC | 480 |
| GTACAGCCAG | CAGTTGACT | GGCGTTACCC | ACCGTCCCCG | CCCCCGCAGC | CAACCCAGTA | 540 |
| CCGTCAACCC | TACGAGGCGT | TGGTGGTAC | CCGGCCGGGT | CTGATACCTG | GCGTGATTCC | 600 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| GACCATGACG | CCCCCTCCTG | GGATGGTTCG | CCAACGCCCT | CGTGCAGGCA | TGTTGGCCAT | 660 |
| CGGCGCGGTG | ACGATAGCGG | TGGTGTCCGC | CGGCATCGGC | GGCGCGGCCG | CATCCCTGGT | 720 |
| CGGGTTCAAC | CGGGCACCCG | CCGGCCCCAG | CGGCGGCCCA | GTGGCTGCCA | GCGCGCGGCC | 780 |
| AAGCATCCCC | GCAGCAAACA | TGCCGCCGGG | GTCGGTCGAA | CAGGTGGCGG | CCAAGGTGGT | 840 |
| GCCCAGTGTC | GTCATGTTGG | AAACCGATCT | GGGCCGCCAG | TCGGAGGAGG | GCTCCGGCAT | 900 |
| CATTCTGTCT | CCCAGAGGGC | TGATCTTGAC | CAACAACCAC | GTGATCGCGG | CGGCCGCCAA | 960 |
| GCCTCCCCTG | GGCAGTCCGC | CGCCGAAAAC | GACGGTAACC | TTCTCTGACG | GGCGGACCGC | 1020 |
| ACCTTTCACG | GTGGTGGGGG | CTGACCCAC | CAGTGATATC | GCCGTCGTCC | GTGTTACAGG | 1080 |
| CGTCTCCGGG | CTCACCCCGA | TCTCCCTGGG | TTCTCTCTCG | GACCTGAGGG | TCGGTCAGCC | 1140 |
| GGTGCTGGCG | ATCGGGTCGC | CGCTCGGTTT | GGAGGGCACC | GTGACCACGG | GGATCGTCAG | 1200 |
| CGCTCTCAAC | CGTCCAGTGT | CGACGACCGG | CGAGGCCGGC | AACCAGAACA | CCGTGCTGGA | 1260 |
| CGCCATTCA | ACCAGCGCCG | CGATCAACCC | CGGTAACCTC | GGGGGCGCGC | TGGTGAACAT | 1320 |
| GAACGCTCAA | CTCGTCGGAG | TCAACTCGGC | CATTGCCACG | CTGGGCGCGG | ACTCAGCCGA | 1380 |
| TGCGCAGAGC | GGCTCGATCG | GTCTCGGTTT | TGCGATTCCA | GTGACACAGG | CCAAGCGCAT | 1440 |
| CGCCGACGAG | TTGATCAGCA | CCGGCAAGGC | GTCACATGCC | TCCCTGGGTG | TGCAGGTGAC | 1500 |
| CAATGACAAA | GACACCCCGG | GCGCCAAGAT | CGTCGAAGTA | GTGGCCGGTG | GTGCTGCCGC | 1560 |
| GAACGCTGGA | GTGCCGAAGG | GCGTCGTTGT | CACCAAGGTC | GACGACCGCC | CGATCAACAG | 1620 |
| CGCGGACGCG | TTGGTTGCCG | CCGTGCGGTC | CAAAGCGCCG | GGCGCCACGG | TGGCGCTAAC | 1680 |
| CTTTCAGGAT | CCCTCGGGCG | GTAGCCGCAC | AGTGCAAGTC | ACCCTCGGCA | AGGCGGAGCA | 1740 |
| GTGATGAAGG | TCGCCGCGCA | GTGTTCAAAG | C | | | 1771 |

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| CTCCACCGCG | GTGGCGGCCG | CTCTAGAACT | AGTGGATCCC | CCGGGCTGCA | GGAATTCGGC | 60 |
| ACGAGGATCC | GACGTGCGAG | GTTGTGCAAC | CCGCCGCCGC | GGAAGTATCG | GTCCATGCCT | 120 |
| AGCCCAGCGA | CGGCGAGCGC | CGGAATGGCG | CGAGTGAGGA | GGCGGGCAAT | TTGGCGGGGC | 180 |
| CCGGCGACGG | CGAGCGCCGG | AATGGCGCGA | GTGAGGAGGC | GGGCAGTCAT | GCCCAGCGTG | 240 |
| ATCCAATCAA | CCTGCATTCT | GCCTGCGGGC | CCATTTGACA | ATCGAGGTAG | TGAGCGCAAA | 300 |
| TGAATGATGG | AAAACGGGCG | GTGACGTCCG | CTGTTCTGGT | GGTGCTAGGT | GCCTGCCTGG | 360 |
| CGTTGTGGCT | ATCAGGATGT | TCTTCGCCGA | AACCTGATGC | CGAGGAACAG | GGTGTTCCCG | 420 |
| TGAGCCCGAC | GGCGTCCGAC | CCCGCGCTCC | TCGCCGAGAT | CAGGCAGTCG | CTTGATGCCA | 480 |
| CAAAAGGGTT | GACCAGCGTG | CACGTAGCGG | TCCGAACAAC | CGGGAAAGTC | GACAGCTTGC | 540 |
| TGGGTATTAC | CAGTGCCGAT | GTGACGTCC | GGGCCAATCC | GCTCGCGGCA | AAGGGCGTAT | 600 |
| GCACCTACAA | CGACGAGCAG | GGTGTCCTCG | TTCGGGTACA | AGGCGACAAC | ATCTCGGTGA | 660 |
| AACTGTTTCA | CGACTGGAGC | AATCTCGGCT | CGATTTCTGA | ACTGTCAACT | TCACGCGTGC | 720 |
| TCGATCCTGC | CGCTGGGGTG | ACGCAGCTGC | TGTCCGGTGT | CACGAACCTC | CAAGCGCAAG | 780 |
| GTACCGAAGT | GATAGACGGA | ATTTGACCA | CCAAAATCAC | CGGGACCATC | CCCGCGAGCT | 840 |
| CTGTCAAGAT | GCTTGATCCT | GGCGCCAAGA | GTGCAAGGCC | GGCGACCGTG | TGGATTGCCC | 900 |
| AGGACGGCTC | GCACCACCTC | GTCCGAGCGA | GCATCGACCT | CGGATCCGGG | TCGATTGAGC | 960 |
| TCACGCGATC | GAAATGGAAC | GAACCCGTCA | ACGTGCACTA | GGCCGAAGTT | GCGTCGACGC | 1020 |
| GTTGNTCGAA | ACGCCCTTGT | GAACGGTGTC | AACGGNAC | | | 1058 |

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAATTCGGCA | CGAGAGGTGA | TCGACATCAT | CGGGACCAGC | CCCACATCGT | GGGAACAGGC | 60 |
| GGCGGCGGAG | GCGGTCCAGC | GGGCGCGGGA | TAGCGTCGAT | GACATCCGCG | TCGCTCGGGT | 120 |
| CATTGAGCAG | GACATGGCCG | TGGACAGCGC | CGGCAAGATC | ACCTACCGCA | TCAAGCTCGA | 180 |
| AGTGTCTGTT | AAGATGAGGC | CGGCGCAACC | GCGCTAGCAC | GGGCCGGCGA | GCAAGACGCA | 240 |
| AAATCGCACG | GTTTGCAGTT | GATTCGTGCG | ATTTTGTGTC | TGCTCGCCGA | GGCCTACCAG | 300 |
| GCGCGGCCCA | GTTCGCGGTG | CTGCCGTATC | CAGGCGTGCA | TCGCGATTCC | GGCGGCCACG | 360 |
| CCGAGATTAA | TGCTTCGCGT | CGACCCGAAC | TGGGCGATCC | GCCGNGAGC | TGATCGATGA | 420 |
| CCGTGGCCAG | CCCGTCGATG | CCCGAGTTGC | CCGAGGAAAC | GTGCTGCCAG | GCCGTTAGGA | 480 |
| AGCGTCCGTA | GGCGGCGGTG | CTGACCGGCT | CTGCCTGCGC | CCTCAGTGCG | GCCAGCGAGC | 540 |
| GG | | | | | | 542 |

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 913 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

| | | | | | | |
|------------|------------|-------------|------------|------------|-------------|-----|
| CGGTGCCGCC | CGCGCCTCCG | TTGCCCCCAT | TGCCGCCGTC | GCCGATCAGC | TGCGCATCGC | 60 |
| CACCATCACC | GCCTTTGCCG | CCGGCACC GC | CGGTGGCGCC | GGGGCCGCCG | ATGCCACCGC | 120 |
| TTGACCCTGG | CCGCCGGCGC | CGCCATTGCC | ATACAGCACC | CCGCCGGGGG | CACCGTTACC | 180 |
| GCCGTCGCCA | CCGTCGCCGC | CGCTGCCGTT | TCAGGCCGGG | GAGGCCGAAT | GAACCGCCGC | 240 |
| CAAGCCCGCC | GCCGGCACC | TTGCCGCCTT | TTCCGCCCGC | CCCGCCGGCG | CCGCCAATTG | 300 |
| CCGAACAGCC | AMGCACCGTT | GCCGCCAGCC | CCGCCGCCGT | TAACGGCGCT | GCCGGGCGCC | 360 |
| GCCGCCGGAC | CCGCCATTAC | CGCCGTTCCC | GTTCGGTGCC | CCGCCGTTAC | CGGCGCCGCC | 420 |
| GTTTGCCGCC | AATATTCGGC | GGGCACCGCC | AGACCCGCCG | GGGCCACCAT | TGCCGCCGGG | 480 |
| CACCGAAACA | ACAGCCCAAC | GGTGCCGCCG | GCCCCGCCGT | TTGCCGCCAT | CACCGGCCAT | 540 |
| TCACCGCCAG | CACCGCCGTT | AATGTTTATG | AACCCGGTAC | CGCCAGCGCG | GCCCCATTATG | 600 |
| CCGGGCGCCG | GAGNGCGTGC | CCGCCGGCGC | CGCCAACGCC | CAAAAGCCCG | GGGTTGCCAC | 660 |
| CGGCCCGGCC | GGACCCACCG | GTCCCGCCGA | TCCCCCGGTT | GCCGCCGGTG | CCGCCGCCAT | 720 |
| TGGTGCTGCT | GAAGCCGTTA | GCGCCGGTTC | CGCSGGTTCC | GGCGGTGGCG | CCNTGGCCGC | 780 |
| CGGCCCGGCC | GTTGCCGTAC | AGCCACCCCC | CGGTGGCGCC | GTTGCCGCCA | TTGCCGCCAT | 840 |
| TGCCGCCGTT | GCCGCCATTG | CCGCCGTTCC | CGCCGCCACC | GCCGGNTTGG | CCGCCGGCGC | 900 |
| CGCCGGCGGC | CGC | | | | | 913 |

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1872 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GACTACGTTG | GTGTAGAAAA | ATCCTGCCGC | CCGGACCCTT | AAGGCTGGGA | CAATTTCTGA | 60 |
| TAGTACCCCC | GACACAGGAG | GTTACGGGAT | GAGCAATTGC | CGCCGCCGCT | CACTCAGGTG | 120 |

GTCATGGTTG CTGAGCGTGC TGGCTGCCGT CGGGCTGGGC CTGGCCACGG CGCCGGCCCA 180
 GCGCGCCCCG CCGGCCTTGT CGCAGGACCG GTTCGCCGAC TTCCCCGCGC TGCCCCCTCGA 240
 CCCGTCCGCG ATGGTCGCCC AAGTGGCGCC ACAGGTGGTC AACATCAACA CCAAACCTGGG 300
 CTACAACAAC GCCGTGGGCG CCGGACCGG CATCGTCATC GATCCCAACG GTGTCTGTGCT 360
 GACCAACAAC CACGTGATCG CGGGCGCCAC CGACATCAAT GCGTTCAGCG TCGGCTCCGG 420
 CCAAACCTAC GCGTTCGATG TGGTCGGGTA TGACCGCACC CAGGATGTCTG CGGTGCTGCA 480
 GCTGCGCGGT GCCGGTGGCC TGCCGTCGGC GCGCATCGGT GGCGGCGTCTG CGGTTGGTGA 540
 GCCCGTCGTC GCGATGGGCA ACAGCGGTGG GCAGGGCGGA ACGCCCCGTG CGGTGCCTGG 600
 CAGGGTGGTC GCGCTCGGCC AAACCGTGCA GCGCTCGGAT TCGCTGACCG GTGCCGAAGA 660
 GACATTGAAC GGGTTGATCC AGTTCGATCG CGCAATCCAG CCCGGTGATT CGGGCGGGCC 720
 CGTCGTCAAC GGCCTAGGAC AGGTGGTCGG TATGAACACG GCCCGTCCG ATAACCTCCA 780
 GCTGTCCAG GGTGGGCAGG GATTCGCCAT TCCGATCGGG CAGGCGATGG CGATCGCGGG 840
 CCAAATCCGA TCGGGTGGGG GGTCAACCCAC CGTTCATATC GGGCCTACCG CCTTCCTCGG 900
 CTTGGGTGTT GTCGACAACA ACGGCAACGG CGCACGAGTC CAACGCGTGG TCGGAAGCGC 960
 TCCGCGGGCA AGTCTCGGCA TCTCCACCGG CGACGTGATC ACCGCGGTCTG ACGGCGCTCC 1020
 GATCAACTCG GCCACCGCGA TGGCGGACGC GCTTAACGGG CATCATCCCG GTGACGTCAT 1080
 CTCGGTGAAC TGGCAAACCA AGTCGGGCGG CACGCGTACA GGAACGTGA CATTGGCCGA 1140
 GGGACCCCCG GCCTGATTTG TCGCGGATAC CACCCGCCGG CCGGCCAATT GGATTGGCGC 1200
 CAGCCGTGAT TGCCCGGTGA GCCCCGAGT TCCGTCTCCC GTGCGCGTGG CATTGTGGAA 1260
 GCAATGAACG AGGCAGAACA CAGCGTTGAG CACCCTCCCG TGCAGGGCAG TTACGTCGAA 1320
 GGCGGTGTGG TCGAGCATCC GGATGCCAAG GACTTCGGCA GCGCCGCCGC CCTGCCCGCC 1380
 GATCCGACCT GGTTTAAGCA CGCCGTCTTC TACGAGGTGC TGGTCCGGGC GTTCTTCGAC 1440
 GCCAGCGCGG ACGGTTCCGN CGATCTGCGT GGACTCATCG ATCGCCTCGA CTACCTGCAG 1500
 TGGCTTGGCA TCGACTGCAT CTGTTGCCCG CGTTCTTACG ACTCACCGCT GCGCGACGGC 1560
 GGTACGACA TTCGCGACTT CTACAAGGTG CTGCCCGAAT TCGGCACCGT CGACGATTTT 1620
 GTCGCCCTGG TCGACACCGC TCACCGGCGA GGTATCCGCA TCATCACCGA CCTGGTGATG 1680
 AATCACACCT CGGAGTCGCA CCCCTGGTTT CAGGAGTCCC GCCGCGACCC AGACGGACCG 1740
 TACGGTGACT ATTACGTGTG GAGCGACACC AGCGAGCGCT ACACCGACGC CCGGATCATC 1800
 TTCGTCGACA CCGAAGAGTC GAACTGGTCA TTCGATCCTG TCCGCCGACA GTTNCTACTG 1860
 GCACCGATTG TT 1872

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTCGCCGAA ACCTGATGCC GAGGAACAGG GTGTTCCCGT GAGCCCGACG GCGTCCGACC 60
 CCGCGCTCCT CGCCGAGATC AGGCAGTCGC TTGATGCGAC AAAAGGGTTG ACCAGCGTGC 120
 ACGTAGCGGT CCGAACAACC GGGAAAGTCG ACAGCTTGCT GGGTATTACC AGTGCCGATG 180
 TCGACGTCCG GGCCAATCCG CTCGCGGCAA AGGGCGTATG CACCTACAAC GACGAGCAGG 240
 GTGTCCCGTT TCGGGTACAA GGCGACAACA TCTCGGTGAA ACTGTTTCGAC GACTGGAGCA 300
 ATCTCGGCTC GATTTCTGAA CTGTCAACTT CACGCGTGCT CGATCCTGCC GCTGGGGTGA 360
 CGCAGCTGCT GTCCGGTGTC ACGAACCTCC AAGCGCAAGG TACCGAAGTG ATAGACGGAA 420
 TTTTCGACCAC CAAAATCACC GGGACCATCC CCGCGAGCTC TGTCAAGATG CTTGATCCTG 480
 GCGCCAAGAG TGCAAGGCCG GCGACCGTGT GGATTGCCCA GGACGGCTCG CACCACCTCG 540
 TCCGAGCGAG CATCGACCTC GGATCCGGGT CGATTGAGCT CACGCGATCG AAATGGAACG 600
 AACCCGTCAA CGTCGACTAG GCCGAAGTTG CGTCGACGCG TTGCTCGAAA CGCCCTTGTTG 660
 AACGGTGTCA ACGGCACCCG AAAACTGACC CCCTGACGGC ATCTGAAAAT TGACCCCTTA 720
 GACCGGGCGG TTGGTGGTTA TTCTTCGGTG GTTCCGGCTG GTGGGACGCG GCCGAGGTCTG 780
 CGGTCCTTTGA GCCGGTAGCT GTCGCCTTTG AGGGCGACGA CTTGAGCATG GTGGACGAGG 840

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| CGGTCGATCA | TGGCGGCAGC | AACGACGTCG | TCGCCGCCGA | AAACCTCGCC | CCACCGGCCG | 900 |
| AAGGCCTTAT | TGGACGTGAC | GATCAAGCTG | GCCCGCTCAT | ACCGGGAGGA | CACCAGCTGG | 960 |
| AAGAAGAGGT | TGGCGGCCTC | GGGCTCAAAC | GGAATGTAAC | CGACTTCGTC | AACCACCAGG | 1020 |
| AGCGGATAGC | GGCCAAACCG | GGTGAGTTCG | GCGTAGATGC | GCCCGGCGTG | GTGAGCCTCG | 1080 |
| GCGAACCGTG | CTACCCATTG | GGCGGCGGTG | GCGAACAGCA | CCCGATGACC | GGCCTGACAC | 1140 |
| GCGCGTATCG | CCAGGCCGAC | CGCAAGATGA | GTCTTCCCGG | TGCCAGGCGG | GGCCCAAAAA | 1200 |
| CACGACGTTA | TCGCGGGCGG | TGATGAAATC | CAGGGTGCCC | AGATGTGCGA | TGGTGTGCGG | 1260 |
| TTTGAGGCCA | CGAGCATGCT | CAAAGTCGAA | CTCTTCCAAC | GACTTCCGAA | CCGGGAAGCG | 1320 |
| GGCGGCGCGG | ATGCGGCCCT | CACCACCATG | GGACTCCCGG | GCTGACACTT | CCCGCTGCAG | 1380 |
| GCAGGCGGCC | AGGTATTCTT | CGTGGCTCCA | GTTCTCGGCG | CGGGCGCGAT | CGGCCAGCCG | 1440 |
| GGACACTGAC | TCACGCAGGG | TGGGAGCTTT | CAATGCTCTT | GT | | 1482 |

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GAATTCGGCA | CGAGCCGGCG | ATAGCTTCTG | GGCCGCGGCC | GACCAGATGG | CTCGAGGGTT | 60 |
| CGTGCTCGGG | GCCACCGCCG | GGCGCACCAC | CCTGACCGGT | GAGGGCCTGC | AACACGCCGA | 120 |
| CGGTCACTCG | TTGCTGCTGG | ACGCCACCAA | CCCggCGGTG | GTTGCCTACG | ACCCGGCCTT | 180 |
| CGCTACGAA | ATCGGCTACA | TCGNNGAAAG | CGGACTGGCC | AGGATGTGCG | GGGAGAACCC | 240 |
| GGAGAACATC | TTCTTCTACA | TCACCGTCTA | CAACGAGCCG | TACGTGCAGC | CGCCGGAGCC | 300 |
| GGAGAACTTC | GATCCCAGAG | GCGTGCTGGG | GGGTATCTAC | CGNTATCAG | CGGCCACCGA | 360 |
| GCAACGCACC | AACAAGNGC | AGATCCTGGC | CTCCGGGGTA | GCGATGCCCG | CGGCGCTGCG | 420 |
| GGCAGCACAG | ATGCTGGCCG | CCGAGTGGGA | TGTCGCCGCC | GACGTGTGGT | CGGTGACCAG | 480 |
| TTGGGGCGAG | CTAAACCGCG | ACGGGGTGGT | CATCGAGACC | GAGAAGCTCC | GCCACCCCGA | 540 |
| TCGGCCGGCG | GGCGTGCCCT | ACGTGACGAG | AGCGCTGGAG | AATGCTCGGG | GCCCGTGAT | 600 |
| CGCGTGTCTG | GACTGGATGC | GCGCGGTCCC | CGAGCAGATC | CGACCGTGGG | TGCCGGGCAC | 660 |
| ATACCTCACG | TTGGGCACCG | ACGGGTTCGG | TTTTTCCGAC | ACTCGGCCCG | CCGGTCGTCTG | 720 |
| TTACTTCAAC | ACCGACGCCG | AATCCCAGGT | TGGTCGCGGT | TTTGGGAGGG | GTGCGCCGGG | 780 |
| TCGACGGGTG | AATATCGACC | CATTGCGTGC | CGGTGCTGGG | CCGCCCGCCC | AGTTACCCGG | 840 |
| ATTCGACGAA | GGTGGGGGGT | TGCGCCCGAN | TAAATT | | | 876 |

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

| | | | | | | |
|------------|------------|------------|------------|-------------|-------------|-----|
| ATCCCCCGCG | GCTGCAGGAA | TTCGGCACGA | GAGACAAAAT | TCCACGCGTT | AATGCAGGAA | 60 |
| CAGATTCATA | ACGAATTCAC | AGCGGCACAA | CAATATGTCG | CGATCGCGGT | TTATTTTCGAC | 120 |
| AGCGAAGACC | TGCCGCAAGT | GGCGAAGCAT | TTTTACAGCC | AAGCGGTCGA | GGAACGAAAC | 180 |
| CATGCAATGA | TGCTCGTGCA | ACACCTGCTC | GACCGCGACC | TTCGTGTGCA | AATTCCCGGC | 240 |
| GTAGACACGG | TGCGAAACCA | GTTGACAGA | CCCCGCGAGG | CACTGGCGCT | GGCGCTCGAT | 300 |
| CAGGAACGCA | CAGTCACCGA | CCAGGTGCGT | CGGCTGACAG | CGGTGGCCCCG | CGACGAGGGC | 360 |
| GATTTCTCTG | GCGAGCAGTT | CATGCAGTGG | TTCTTGACAG | AACAGATCGA | AGAGGTGGCC | 420 |

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|------|
| TTGATGGCAA | CCCTGGTGCG | GGTTGCCGAT | CGGGCCGGGG | CCAACCTGTT | CGAGCTAGAG | 480 |
| AACTTCGTCT | CACGTGAAGT | GGATGTGGCG | CCGGCCGCAT | CAGGCGCCCC | GCACGCTGCC | 540 |
| GGGGGCCGCC | TCTAGATCCC | TGGGGGGGAT | CAGCGAGTGG | TCCCGTTTCG | CCGCCCCGTCT | 600 |
| TCCAGCCAGG | CCTTGGTGCG | GCCGGGGTGG | TGAGTACCAA | TCCAGGCCAC | CCCGACCTCC | 660 |
| CGGNAAAAGT | CGATGTCTCT | GTACTCATCG | ACGTTCCAGG | AGTACACCGC | CCGGCCCTGA | 720 |
| GCTGCCGAGC | GGTCAACGAG | TTGCGGATAT | TCCTTTAACG | CAGGCAGTGA | GGGTCCCACG | 780 |
| GCGGTTGGCC | CGACCGCCGT | GGCCGCACTG | CTGGTCAGGT | ATCGGGGGGT | CTTGGCGAGC | 840 |
| AACAACGTCG | GCAGGAGGGG | TGGAGCCCGC | CGGATCCGCA | GACCGGGGGG | GCGAAAACGA | 900 |
| CATCAACACC | GCACGGGATC | GATCTGCGGA | GGGGGGTTCG | GGAATACCGA | ACCGGTGTAG | 960 |
| GAGCGCCAGC | AGTTGTTTTT | CCACCAGCGA | AGCGTTTTTC | GGTCATCGGN | GGCNNTTAAG | 1020 |
| T | | | | | | 1021 |

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| CGTGCCGACG | AACGGAAGAA | CACAACCATG | AAGATGGTGA | AATCGATCGC | CGCAGGTCTG | 60 |
| ACCGCCGCGG | CTGCAATCGG | CGCCGCTGCG | GCCGGTGTGA | CTTCGATCAT | GGCTGGCGGN | 120 |
| CCGGTCGTAT | ACCAGATGCA | GCCGGTCGTC | TTCGGCGCGC | CACTGCCGTT | GGACCCGNA | 180 |
| TCCGCCCCTG | ANGTCCCGAC | CGCCGCCCCG | TGGACCAGNC | TGCTCAACAG | NCTCGNCGAT | 240 |
| CCCAACGTGT | CGTTTGNAA | CAAGGGNAGT | CTGGTCGAGG | GNGGNATCGG | NNGGNANCGAG | 300 |
| GNGNGNATC | GNCGANCA | A | | | | 321 |

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TCTTATCGGT | TCCGGTTGGC | GACGGGTTTT | GGGNGCGGGT | GGTTAACCCG | CTCGGCCAGC | 60 |
| CGATCGACGG | GCGCGGAGAC | GTCGACTCCG | ATACTCGGCG | CGCGCTGGAG | CTCCAGGCGC | 120 |
| CCTCGGTGGT | GNACCGGCAA | GCGGTGAAGG | AGCCGTTGNA | GACCGGGATC | AAGGCGATTG | 180 |
| ACGCGATGAC | CCCAGTCGGC | CGCGGGCAGC | GCCAGCTGAT | CATCGGGGAC | CGCAAGACCG | 240 |
| GCAAAAACCG | CCGTCTGTGT | CGGACACCAT | CCTCAAACCA | GCGGGAAGAA | CTGGGAGTCC | 300 |
| GGTGGATCCC | AAGAAGCAGG | TGCGCTTGTG | TATACGTTGG | CCATCGGGCA | AGAAGGGGAA | 360 |
| CTTACCATCG | CCG | | | | | 373 |

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTGACGCCGT | GATGGGATTC | CTGGGCGGGG | CCGGTCCGCT | GGCGGTGGTG | GATCAGCAAC | 60 |
| TGGTTACCCG | GGTGCCGCAA | GGCTGGTCGT | TTGCTCAGGC | AGCCGCTGTG | CCGGTGGTGT | 120 |
| TCTTGACGGC | CTGGTACGGG | TTGGCCGATT | TAGCCGAGAT | CAAGGCGGGC | GAATCGGTGC | 180 |
| TGATCCATGC | CGGTACCGGC | GGTGTGGGCA | TGGCGGCTGT | GCAGCTGGGT | CGCCAGTGGG | 240 |
| GCGTGGAGGT | TTTCGTCACC | GCCAGCCGTG | GNAAGTGGGA | CACGCTGCGC | GCCATNGNGT | 300 |
| TTGACGACGA | NCCATATCGG | NGATTCCNC | ACATNCGAAG | TTCCGANGGA | GA | 352 |

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|-----|
| GAAATCCGCG | TTCATTCCGT | TCGACCAGCG | GCTGGCGATA | ATCGACGAAG | TGATCAAGCC | 60 |
| GCGGTTCCGCG | GCGCTCATGG | GTCACAGCGA | GTAATCAGCA | AGTTCTCTGG | TATATCGCAC | 120 |
| CTAGCGTCCA | GTTGCTTGCC | AGATCGCTTT | CGTACCGTCA | TCGCATGTAC | CGGTTCCGCGT | 180 |
| GCCGCACGCT | CATGCTGGCG | GCGTGCATCC | TGGCCACGGG | TGTGGCGGGT | CTCGGGGTCTG | 240 |
| GCGCGCAGTC | CGCAGCCCAA | ACCGCGCCGG | TGCCCGACTA | CTACTGGTGC | CCGGGGCAGC | 300 |
| CTTTTCGACCC | CGCATGGGGG | CCCAACTGGG | ATCCCTACAC | CTGCCATGAC | GACTTCCACC | 360 |
| GCGACAGCGA | CGGCCCCGAC | CACAGCCGCG | ACTACCCCGG | ACCCATCCTC | GAAGGTCCCG | 420 |
| TGCTTGACGA | TCCCGGTGCT | GCGCCGCCGC | CCCCGGCTGC | CGGTGGCGGC | GCATAGCGCT | 480 |
| CGTTGACCGG | GCCGCATCAG | CGAATACGCG | TATAAACCCG | GGCGTGCCCC | CGGCAAGCTA | 540 |
| CGACCCCGG | CGGGGCAGAT | TTACGCTCCC | GTGCCGATGG | ATCGCGCCGT | CCGATGACAG | 600 |
| AAAATAGGCG | ACGGTTTGG | CAACCGCTTG | GAGGACGCTT | GAAGGGAACC | TGTCATGAAC | 660 |
| GGCGACAGCG | CCTCCACCAT | CGACATCGAC | AAGGTTGTTA | CCCGCACACC | CGTTCGCCGG | 720 |
| ATCGTG | | | | | | 726 |

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

| | | | | | | |
|-------------|-------------|------------|------------|------------|------------|-----|
| CGCGACGACG | ACGAACGTCG | GGCCCACCAC | CGCCTATGCG | TTGATGCAGG | CGACCGGGAT | 60 |
| GGTCGCCGAC | CATATCCAAG | CATGCTGGGT | GCCCACTGAG | CGACCTTTTG | ACCAGCCGGG | 120 |
| CTGCCCCGATG | GCGGCCCCGGT | GAAGTCATTG | CGCCGGGGCT | TGTGCACCTG | ATGAACCCGA | 180 |
| ATAGGGAACA | ATAGGGGGGT | GATTTGGCAG | TTCAATGTCG | GGTATGGCTG | GAAATCCAAT | 240 |
| GGCGGGGCAT | GCTCGGCGCC | GACCAGGCTC | GCGCAGGCGG | GCCAGCCCCA | ATCTGGAGGG | 300 |
| AGCACTCAAT | GGCGGCGATG | AAGCCCCGGA | CCGGCGACGG | TCCTTTGGAA | GCAACTAAGG | 360 |
| AGGGGCGCGG | CATTGTGATG | CGAGTACCAC | TTGAGGGTGG | CGGTCGCCTG | GTCGTCGAGC | 420 |
| TGACACCCGA | CGAAGCCGCC | GCACTGGGTG | ACGAACTCAA | AGGCGTTACT | AGCTAAGACC | 480 |
| AGCCCCACGG | CGAATGGTCG | GCGTTACGCG | CACACCTTCC | GGTAGATGTC | CAGTGTCTGC | 540 |
| TCGGCGATGT | ATGCCCAGGA | GAACTCTTGG | ATACAGCGCT | | | 580 |

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AACGGAGGCG | CCGGGGGTTT | TGGCGGGGCC | GGGCGGTTCG | GCGGCAACGG | CGGGGCCGGC | 60 |
| GGTACCGCCG | GGTTGTTCGG | TGTCGGCGGG | GCCGGTGGGG | CCGGAGGCAA | CGGCATCGCC | 120 |
| GGTGTACCG | GTACGTCGGC | CAGCACACCG | GGTGGATCCG | | | 160 |

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GACACCGATA | CGATGGTGAT | GTACGCCAAC | GTTGTCGACA | CGCTCGAGGC | G TTCACGATC | 60 |
| CAGCGCACAC | CCGACGGCGT | GACCATCGGC | GATGCGGCC | CGTTCGCGGA | GGCGGCTGCC | 120 |
| AAGGCGATGG | GAATCGACAA | GCTGCGGGTA | ATTCATACCG | GAATGGACCC | CGTCGTCGCT | 180 |
| GAACGCGAAC | AGTGGGACGA | CGGCAACAAC | ACGTTGGCGT | TGGCGCCCGG | TGTCGTTGTC | 240 |
| GCCTACGAGC | GCAACGTACA | GACCAACGCC | CG | | | 272 |

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GCAGCCGGTG | GTTCTCGGAC | TATCTGCGCA | CGGTGACGCA | GCGCGACGTG | CGCGAGCTGA | 60 |
| AGCGGATCGA | GCAGACGGAT | CGCCTGCCGC | GGTTCATGCG | CTACCTGGCC | GCTATCACCG | 120 |
| CGCAGGAGCT | GAACGTGGCC | GAAGCGGCGC | GGGTCATCGG | GGTCGACGCG | GGGACGATCC | 180 |
| GTTTCGGATCT | GGCGTGGTTC | GAGACGGTCT | ATCTGGTACA | TCGCCTGCCC | GCCTGGTCGC | 240 |
| GGAATCTGAC | CGCGAAGATC | AAGAAGCGGT | CAAAGATCCA | CGTCGTCGAC | AGTGGCTTCG | 300 |
| CGGCCTGGTT | GCGCGGG | | | | | 317 |

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| GATCGTGGAG | CTGTCTGATGA | ACAGCGTTGC | CGGACGCGCG | GCGGCCAGCA | CGTCGGTGTA | 60 |
| GCAGCGCCGG | ACCACCTCGC | CGGTGGGCAG | CATGGTGATG | ACCACGTCGG | CCTCGGCCAC | 120 |
| CGCTTCGGGC | GCGCTACGAA | ACACCGCGAC | ACCGTGCGCG | GCGGCGCCGG | ACGCCGCCGT | 180 |
| GG | | | | | | 182 |

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

| | | | | | | |
|------------|------------|-------------|------------|-------------|------------|-----|
| GATCGCGAAG | TTTGGTGAGC | AGGTGGTCTGA | CGCGAAAGTC | TGGGCGCCTG | CGAAGCGGGT | 60 |
| CGGCGTTCAC | GAGGCGAAGA | CACGCCTGTC | CGAGCTGCTG | CGGCTCGTCT | ACGGCGGGCA | 120 |
| GAGGTTGAGA | TTGCCCGCCG | CGGCGAGCCG | GTAACAAAGC | TTGTGCCGCT | GCATCCTCAT | 180 |
| GAGACTCGGC | GGTTAGGCAT | TGACCATGGC | GTGTACCGCG | TGCCCCGACGA | TTTGGACGCT | 240 |
| CCGTTGTGAG | ACGACGTGCT | CGAACGCTTT | CACCGGTGAA | GCGCTACCTC | ATCGACACCC | 300 |
| ACGTTTGG | | | | | | 308 |

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCGACGACGA | GCAACTCACG | TGGATGATGG | TCGGCAGCGG | CATTGAGGAC | GGAGAGAATC | 60 |
| CGGCCGAAGC | TGCCGCGCGG | CAAGTGCTCA | TAGTGACCGG | CCGTAGAGGG | CTCCCCGAT | 120 |
| GACACCGGAC | TATTCTGGTG | TGCCGCTGGC | CGGTAAGAGC | GGGTAAAAGA | ATGTGAGGGG | 180 |
| ACACGATGAG | TAATCACACC | TACCGAGTGA | TCGAGATCGT | CGGGACCTCG | CCCACGGCG | 240 |
| TCGACGCGGC | AATCCAGGGC | GGTCTGG | | | | 267 |

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

| | | | | | | |
|------------|------------|-------------|------------|-------------|-------------|-----|
| CTCGTGCCGA | AAGAATGTGA | GGGGACACGA | TGAGCAATCA | CACCTACCGA | GTGATCGAGA | 60 |
| TCGTCGGGAC | CTCGCCCGAC | GGCGTCGACG | CGGCAATCCA | GGGCGGTCTG | GCCCGAGCTG | 120 |
| CGCAGACCAT | GCGCGCGCTG | GACTGGTTTCG | AAGTACAGTC | AATTCGAGGC | CACCTGGTCTG | 180 |
| ACGAGCGGT | CGCGCACTTC | CAGGTGACTA | TGAAAGTCGG | CTTCGCTGG | AGGATTCCTG | 240 |
| AACCTTCAAG | CGCGCCGAT | AACTGAGGTG | CATCATTAAG | CGACTTTTCC | AGAACATCCT | 300 |
| GACGCGCTCG | AAACGCGGTT | CAGCCGACGG | TGGCTCCGCC | GAGGCGCTGC | CTCCAAAATC | 360 |
| CCTGCGACAA | TTCTGTCGGC | GCGCCTACAA | GGAAGTCGGT | GCTGAATTCTG | TCGGGTATCT | 420 |

GGTCGACCTG TGTGGGCTGC AGCCGGACGA AGCGGTGCTC GACGTCGGCT GCGGCTCGGG 480
 GCGGATGGCG TTGCCGCTCA CCGGCTATCT GAACAGCGAG GGACGCTACG CCGGCTTCGA 540
 TATCTCGCAG AAAGCCATCG CGTGGTGCCA GGAGCACATC ACCTCGGCGC ACCCCAATT 600
 CCAGTTCGAG GTCTCCGACA TCTACAATC GCTGTACAAC CCGAAAGGGA AATACCAGTC 660
 ACTAGACTTT CGCTTTCCAT ATCCGGATGC GTCGTTTCGAT GTGGTGTTTC TTACCTCGGT 720
 GTTACCCAC ATGTTTCCGC CGGACGTGGA GCACTATCTG GACGAGATCT CCCGCGTGCT 780
 GAAGCCCGGC GGACGATGCC TGTGCACGTA CTTCTTGCTC AATGACGAGT CGTTAGCCCA 840
 CATCGCGGAA GGAAAGAGTG CGCACAATT CCAGCATGAG GGACCGGGTT ATCGGACAAT 900
 CCACAAGAAG CGGCCCGAAG AAGCAATCGG CTTGCCGGAG ACCTTCGTCA GGGATGTCTA 960
 TGGCAAGTTC GGCCTCGCCG TGCACGAACC ATTGCACTAC GGCTCATGGA GTGGCCGGGA 1020
 ACCACGCCTA AGCTTCCAGG ACATCGTCAT CGCGACCAA ACCGCGAGCT AGGTCCGCAT 1080
 CCGGGAAGCA TCGCGACACC GTGGCGCCGA GCGCCGCTGC CGGCAGGCCG ATTAGCGGG 1140
 CAGATTAGCC CGCCGCGGCT CCCGGCTCCG AGTACGGCGC CCCGAATGGC GTCACCGGCT 1200
 GGTAACCACG CTTGCGCGCC TGGGCGGCGG CCTGCCGGAT CAGGTGGTAG ATGCCGACAA 1260
 AGCCTGCGTG ATCGGTCATC ACCAACGGTG ACAGCAGCCG GTTGTGCACC AGCGCGAACG 1320
 CCACCCCGGT CTCCGGGTCT GTCCAGCCGA TCGAGCCGCC CAAGCCCACA TGACCAAACC 1380
 CCGGCATCAC GTTGCCGATC GGCATACCGT GATAGCCAAG ATGAAAATTT AAGGGCACCA 1440
 ATAGATTTCG ATCCGGCAGA ACTTGCCGTC GGTTCGCGGT CAGGCCCGTG ACCAGCTCCC 1500
 GCGACAAGAA CCGTATGCCG TCGATCTCGC CTCGTGCCG 1539

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGCAGGGTG GCGTGGATGA GCGTCACCGC GGGGCAGGCC GAGCTGACCG CCGCCCAGGT 60
 CCGGTTGCT GCGGCGGCCT ACGAGACGGC GTATGGGCTG ACGGTGCCCC CGCCGGTGAT 120
 CGCCGAGAAC CGTGCTGAAC TGATGATTCT GATAGCGACC AACCTCTTGG GGCAAAACAC 180
 CCCGGCGATC GCGGTCAACG AGGCCGAATA CGGCGAGATG TGGGCCCAAG ACGCCGCCGC 240
 GATGTTTGGC TACGCCCGCG CGACGGCGAC GGCAGCGGC ACGTTGCTGC CGTTCGAGGA 300
 GGCGCCGGAG ATGACCAGCG CGGGTGGGCT CCTCGAGCAG GCCGCCGCGG TCGAGGAGGC 360
 CTCCGACACC GCCGCGGCGA ACCAGTTGAT GAACAATGTG CCCCAGGCGC TGAACAGTT 420
 GGCCCAAGCC ACGCAGGGCA CCACGCCCTT TTCCAAGCTG GGTGGCCTGT GGAAGACGGT 480
 CTCGCCGCAT CGGTCGCCGA TCAGCAACAT GGTGTGATG GCCAACAACC ACATGTCGAT 540
 GACCAACTCG GGTGTGTCGA TGACCAACAC CTTGAGCTCG ATGTTGAAGG GCTTTGCTCC 600
 GGCGCCGGCC GCCCAGGCCG TGCAAACCGC GGCACAAAAC GGGGTCCGGG CGATGAGCTC 660
 GCTGGGCAGC TCGCTGGGTT CTTCCGGTCT GGGCGGTGGG GTGGCCGCCA ACTTGGGTCTG 720
 GGCGCCCTCG GTACGGTATG GTCACCGGGA TGGCGGAAAA TATGCANAGT CTGGTCGGCG 780
 GAACGGTGGT CCGGCGTAAG GTTACCCCC GTTTTCTGGA TGCGGTGAAC TTCGTCAACG 840
 GAAACAGTTA C 851

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GATCGATCGG | GCGGAAATTT | GGACCAGATT | CGCCTCCGGC | GATAACCCAA | TCAATCGAAC | 60 |
| CTAGATTTAT | TCCGTCCAGG | GGCCCGAGTA | ATGGCTCGCA | GGAGAGGAAC | CTTACTGCTG | 120 |
| CGGGCACCTG | TCGTAGGTCC | TCGATACGGC | GGAAGGCGTC | GACATTTTCC | ACCGACACCC | 180 |
| CCATCCAAAC | GTTTCGAGGC | CACTCCAGCT | TGTGAGCGAG | GCGACGCAGT | CGCAGGCTGC | 240 |
| GCTTGGTCAA | GATC | | | | | 254 |

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| GATCCTGACC | GAAGCGGCCG | CCGCCAAGGC | GAAGTCGCTG | TTGGACCAGG | AGGGACGGGA | 60 |
| CGATCTGGCG | CTGCGGATCG | CGGTTAGCC | GGGGGGGTGC | GCTGGATTGC | GCTATAACCT | 120 |
| TTTCTTCGAC | GACCGGACGC | TGGATGGTGA | CCAAACCGCG | GAGTTCGGTG | GTGTCAGGTT | 180 |
| GATCGTGGAC | CGGATGAGCG | CGCCGTATGT | GGAAGGCGCG | TCGATCGATT | TCGTCGACAC | 240 |
| TATTGAGAAG | CAAGGTTTAC | CATCGACAAT | CCCAACGCCA | CCGGCTCCTG | CGCGTGCGGG | 300 |
| GATTCGTTCA | ACTGATAAAA | CGCTAGTACG | ACCCCGCGGT | GCGCAACACG | TACGAGCACA | 360 |
| CCAAGACCTG | ACCGCGCTGG | AAAAGCAACT | GAGCGATGCC | TTGCACCTGA | CCGCGTGGCG | 420 |
| GGCCGCCGGC | GGCAGGTGTC | ACCTGCATGG | TGAACAGCAC | CTGGGCCTGA | TATTGCGACC | 480 |
| AGTACACGAT | TTTGTGCATC | GAGGTCACCT | CGACCTGGGA | GAACTGCTTG | CGGAACGCGT | 540 |
| CGCTGCTCAG | CTTGGCCAAG | GCCTGATCGG | AGCGCTTGTC | GCGCACGCCG | TCGTGGATAC | 600 |
| CGCACAGCGC | ATTGCGAACG | ATGGTGTCCA | CATCGCGGTT | CTCCAGCGCG | TTGAGGTATC | 660 |
| CCTGAATCGC | GGTTTTGGCC | GGTCCCTCCG | AGAATGTGCC | TGCCGTGTTG | GCTCCGTTGG | 720 |
| TGCGGACCCC | GTATATGATC | GCCGCCGTCA | TAGCCGACAC | CAGCGCGAGG | GCTACCACAA | 780 |
| TGCCGATCAG | CAGCCGCTTG | TGCCGTGCTG | TCGGGTAGGA | CACCTGCGGC | GGCACGCCGG | 840 |
| GATATGCGGC | GGGCGGCAGC | GCCGCGTCGT | CTGCCGGTCC | CGGGGCGAAG | GCCGGTTCGG | 900 |
| CGGCGCCGAG | GTCGTGGGGG | TAGTCCAGGG | CTTGGGGTTC | GTGGGATGAG | GGCTCGGGGT | 960 |
| ACGGCGCCGG | TCCGTTGGTG | CCGACACCGG | GGTTCGGCGA | GTGGGGACCG | GGCATTGTGG | 1020 |
| TTCTCCTAGG | GTGGTGGACG | GGACCAGCTG | CTAGGGCGAC | AACCGCCCGT | CGCGTCAGCC | 1080 |
| GGCAGCATCG | GCAATCAGGT | GAGCTCCCTA | GGCAGGCTAG | CGCAACAGCT | GCCGTCAGCT | 1140 |
| CTCAACGCGA | CGGGGCGGGC | CGCGGCGCCG | ATAATGTTGA | AAGACTAGGC | AACCTTAGGA | 1200 |
| ACGAAGGACG | GAGATTTTGT | GACGATC | | | | 1227 |

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCGGTGTCGG | CGGATCCGGC | GGGTGGTTGA | ACGGCAACGG | CGGGGCCGGC | GGGGCCGGCG | 60 |
| GGACCGGCGC | TAACGGTGGT | GCCGGCGGCA | ACGCCTGGTT | GTTCGGGGCC | GGCGGGTCCG | 120 |
| GCGGNGCCGG | CACCAATGGT | GGNGTCGGCG | GGTCCGGCGG | ATTTGTCTAC | GGCAACGGCG | 180 |
| G | | | | | | 181 |

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

GCGGTGTCGG CGGATCCGGC GGGTGGTTGA ACGGCAACGG CGGTGTCGGC GGCCGGGGCG      60
GCGACGGCGT CTTTGCCGGT GCCGGCGGCC AGGGCGGCCT CGGTGGGCAG GGCGGCAATG      120
GCGGCGGCTC CACCGGCGGC AACGGCGGTC TTGGCGGCGC GGGCGGTGGC GGAGGCAACG      180
CCCCGGACGG CGGCTTCGGT GGCAACGGCG GTAAGGGTGG CCAGGGCGGN ATTGGCGGCG      240
GCACTCAGAG CGCGACCGGC CTCGGNGGTG ACGGCGGTGA CGGCGGTGAC      290

```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

GATCCAGTGG CATGGNGGGT GTCAGTGGA GCAT      34

```

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

GATCGCTGCT CGTCCCCCCC TTGCCGCCGA CGCCACCGGT CCCACCGTTA CCGAACAAGC      60
TGGCGTGGTC GCCAGACCCC CCGGCACCGC CGACGCCGGA GTCGAACAAT GGCACCGTCG      120
TATCCCCACC ATTGCCGCCG GNCCCACCGG CACCG      155

```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

ATGGCGTTCA CGGGGCGCCG GGGACCGGGC AGCCCGNGG GGCCGGGGGG TGG      53

```

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

| | |
|--|-----|
| GATCCACCGC GGGTGCAGAC GGTGCCCCGCG GCGCCACCCC GACCAGCGGC GGCAACGGCG | 60 |
| GCACCGGCGG CAACGGCGCG AACGCCACCG TCGTCGGNGG GGCCGGCGGG GCCGGCGGCA | 120 |
| AGGGCGGCAA CG | 132 |

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

| | |
|---|-----|
| GATCGGCGGC CGGNACGGNC GGGGACGGCG GCAAGGGCGG NAACGGGGGC GCCGNAGCCA | 60 |
| CCNGCCAAGA ATCCTCCGNG TCCNCCAATG GCGCGAATGG CGGACAGGGC GGCAACGGCG | 120 |
| GCANCGGCGG CA | 132 |

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

| | |
|---|-----|
| CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCCG ATTCGCCGGG TTTCCCCACC | 60 |
| CGAGGAAAGC CGTACCAGA TGGCGCTGCC GAAGTAGGGC GATCCGTTTCG CGATGCCGGC | 120 |
| ATGAACGGGC GGCATCAAT TAGTGCAGGA ACCTTTCAGT TTAGCGACGA TAATGGCTAT | 180 |
| AGCACTAAGG AGGATGATCC GATATGACGC AGTCGCAGAC CGTGACGGTG GATCAGCAAG | 240 |
| AGATTTTGA CAGGGCCAAC GAGGTGGAGG CCCCAGTGGC GGACCCACCG ACTGATGTCC | 300 |
| CCATCACACC GTGCGAATC ACGGNGGNTA AAAACGCCGC CCAACAGNTG GTNTTGTCCG | 360 |
| CCGACAACAT GCGGGAATAC CTGGCGGCCG GTGCCAAAGA GCGGCAGCGT CTGGCGACCT | 420 |
| CGCTGCGCAA CGCGGCCAAG GNGTATGGCG AGGTTGATGA GGAGGCTGCG ACCGCGCTGG | 480 |
| ACAACGACGG CGAAGGAAT GTGCAGGCAG AATCGGCCCG GGCCGTCGGA GGGGACAGTT | 540 |
| CGGCCGAAT AACCAGATCG CCGAGGGTGG CCACGGCCCG TGAACCCAAC TTCATGGATC | 600 |
| TCAAAGAAGC GGCAAGGAAG CTCGAAACGG GCGACCAAGG CGCATCGCTC GCGCACTGNG | 660 |
| GGGATGGGTG GAACACTTNC ACCCTGACGC TGCAAGGCGA CG | 702 |

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAAGCCGCAG | CGCTGTCGGG | CGACGTGGCG | GTCAAAGCGG | CATCGCTCGG | TGGCGGTGGA | 60 |
| GGCGGCGGGG | TGCCGTCGGC | GCCGTTGGGA | TCCGCGATCG | GGGGCGCCGA | ATCGGTGCGG | 120 |
| CCCCTGCGG | CTGGTGACAT | TGCCGGCTTA | GGCCAGGGAA | GGGCCGCGG | CGGCGCCGCG | 180 |
| CTGGGCGGCG | GTGGCATGGG | AATGCCGATG | GGTGCCGCGC | ATCAGGGACA | AGGGGGCGCC | 240 |
| AAGTCCAAGG | GTTCTCAGCA | GGAAGACGAG | GCGCTCTACA | CCGAGGATCC | TCGTGCCG | 298 |

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|------|
| CGGCACGAGG | ATCGAATCGC | GTCGCCGGGA | GCACAGCGTC | GCACTGCACC | AGTGGAGGAG | 60 |
| CCATGACCTA | CTCGCCGGGT | AACCCCGGAT | ACCCGCAAGC | GCAGCCCGCA | GGCTCCTACG | 120 |
| GAGGCGTCAC | ACCTCTGTTT | GCCACGCCG | ATGAGGGTGC | GAGCAAGCTA | CCGATGTACC | 180 |
| TGAACATCGC | GGTGGCAGTG | CTCGGTCTGG | CTGCGTACTT | CGCCAGCTTC | GGCCCAATGT | 240 |
| TCACCTCAG | TACCGAACTC | GGGGGGGGTG | ATGGCGCAGT | GTCCGGTGAC | ACTGGGCTGC | 300 |
| CGGTCGGGGT | GGCTCTGCTG | GCTGCGCTGC | TTGCCGGGGT | GGTTCTGGTG | CCTAAGGCCA | 360 |
| AGAGCCATGT | GACGGTAGTT | GCGGTGCTCG | GGGTACTCGG | CGTATTTCTG | ATGGTCTCGG | 420 |
| CGACGTTTAA | CAAGCCCAGC | GCTTATTCGA | CCGGTTGGGC | ATTGTGGGTT | GTGTTGGCTT | 480 |
| TCATCGTGT | CCAGGCGGTT | GCGGCAGTCC | TGGCGCTCTT | GGTGGAGACC | GGCGCTATCA | 540 |
| CCGCGCCGCG | GCCGCGGCCC | AAGTTCGACC | CGTATGGACA | GTACGGGCGG | TACGGGCAGT | 600 |
| ACGGGACAGT | CGGGGTGCAG | CCGGGTGGGT | ACTACGGTCA | GCAGGGTGCT | CAGCAGGCCG | 660 |
| CGGGACTGCA | GTCGCCCGGC | CCGCAGCAGT | CTCCGCAGCC | TCCCGGATAT | GGGTCGCAGT | 720 |
| ACGGCGGCTA | TTCGTCCAGT | CCGAGCCAAT | CGGGCAGTGG | ATACACTGCT | CAGCCCCCGG | 780 |
| CCCAGCCGCC | GGCGCAGTCC | GGGTCGCAAC | AATCGCACCA | GGGCCCATCC | ACGCCACCTA | 840 |
| CCGGCTTTCC | GAGCTTCAGC | CCACCACAC | CGGTCACTGC | CGGGACGGGG | TCGCAGGCTG | 900 |
| GTTTCGGCTCC | AGTCAACTAT | TCAAACCCCA | GCGGGGGCGA | GCAGTCGTCT | TCCCCCGGGG | 960 |
| GGGCGCCGGT | CTAACCAGGC | GTTCCCGCGT | CCGGTCGCGC | GTGTGCGCGA | AGAGTGAACA | 1020 |
| GGGTGTCAGC | AAGCGCGGAC | GATCCTCGTG | CCGAATTC | | | 1058 |

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGGCACGAGA | GACCGATGCC | GCTACCCTCG | CGCAGGAGGC | AGGTAATTTT | GAGCGGATCT | 60 |
| CCGGCGACCT | GAAAACCCAG | ATCGACCAGG | TGGAGTCGAC | GGCAGGTTTC | TTGCAGGGCC | 120 |
| AGTGGCGCGG | CGCGGCGGGG | ACGGCCGCCC | AGGCCGCGGT | GGTGCCTTTC | CAAGAAGCAG | 180 |
| CCAATAAGCA | GAAGCAGGAA | CTCGACGAGA | TCTCGACGAA | TATTCGTCTC | GCCGGCGTCC | 240 |
| AATACTCGAG | GGCCGACGAG | GAGCAGCAGC | AGGCCGCTGT | CTCGCAAATG | GGCTTCTGAC | 300 |
| CCGCTAATAC | GAAAAGAAAC | GGAGCAA | | | | 327 |

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

| | |
|---|-----|
| CGGTCGCGAT GATGGCGTTG TCGAACGTGA CCGATTCTGT ACCGCCGTCG TTGAGATCAA | 60 |
| CCAACAACGT GTTGGCGTCG GCAAATGTGC CGNACCCGTG GATCTCGGTG ATCTTGTCT | 120 |
| TCTTCATCAG GAAGTGCACA CCGGCCACCC TGCCCTCGGN TACCTTTCGG | 170 |

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

| | |
|---|-----|
| GATCCGGCGG CACGGGGGGT GCCGGCGGCA GCACCGCTGG CGCTGGCGGC AACGGCGGGG | 60 |
| CCGGGGGTGG CGGCGGAACC GGTGGGTGTC TCTTCGGCAA CGGCGGTGCC GGCGGGCAGC | 120 |
| GGGCCGT | 127 |

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

| | |
|---|----|
| CGGCGGCAAG GGCGGCACCG CCGGCAACGG GAGCGGCGCG GCCGGCGGCA ACGGCGGCAA | 60 |
| CGGCGGCTCC GGCCTCAACG G | 81 |

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

| | |
|---|-----|
| GATCAGGGCT GGCCGGCTCC GGCCAGAAGG GCGGTAACGG AGGAGCTGCC GGATTGTTTG | 60 |
| GCAACGGCGG GGCCGGNGGT GCCGGCGCGT CCAACCAAGC CGGTAACGGC GGNGCCGGCG | 120 |
| GAAACGGTGG TGCCGGTGGG CTGATCTGG | 149 |

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

| | |
|---|-----|
| CGGCACGAGA TCACACCTAC CGAGTGATCG AGATCGTCGG GACCTCGCCC GACGGTGTCG | 60 |
| ACGCGGNAAT CCAGGGCGGT CTGGCCCGAG CTGCGCAGAC CATGCGCGCG CTGGACTGGT | 120 |
| TCGAAGTACA GTCAATTCGA GGCCACCTGG TCGACGGAGC GGTCGCGCAC TTCCAGGTGA | 180 |
| CTATGAAAGT CGGCTTCCGC CTGGAGGATT CCTGAACCTT CAAGCGCGGC CGATAACTGA | 240 |
| GGTGCATCAT TAAGCGACTT TTCCAGAACA TCCTGACGCG CTCGAAACGC GGTTGAGCCG | 300 |
| ACGGTGGCTC CGCCGAGGCG CTGCCTCCAA AATCCCTGCG ACAATTCGTC GCGCG | 355 |

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

| | |
|--|-----|
| ATGCATCACC ATCACCATCA CATGCATCAG GTGGACCCCA ACTTGACACG TCGCAAGGGA | 60 |
| CGATTGGCGG CACTGGCTAT CGCGGCGATG GCCAGCGCCA GCCTGGTGAC CGTTGCGGTG | 120 |
| CCCGCGACCG CCAACGCCGA TCCGGAGCCA GCGCCCCCGG TACCCACAAC GGCCGCCTCG | 180 |
| CCGCCGTCGA CCGCTGCAGC GCCACCCGCA CCGGCGACAC CTGTTGCCCC CCCACCACCG | 240 |
| GCCGCCGCCA ACACGCCGAA TGCCAGCCG GGCGATCCCA ACGCAGCACC TCCGCCGGCC | 300 |
| GACCCGAACG CACCGCCGCC ACCTGTCTAT GCCCCAAACG CACCCCAACC TGTCCGGATC | 360 |
| GACAACCCGG TTGGAGGATT CAGCTTCGCG CTGCCTGCTG GCTGGGTGGA GTCTGACGCC | 420 |
| GCCCCATTTC ACTACGGTTC AGCACTCCTC AGCAAAACCA CCGGGGACCC GCCATTTCCTC | 480 |
| GGACAGCCGC CGCCGGTGGC CAATGACACC CGTATCGTGC TCGGCCGGCT AGACCAAAAG | 540 |
| CTTTACGCCA GCGCCGAAGC CACCGACTCC AAGGCCGCGG CCCGGTTGGG CTCGGACATG | 600 |
| GGTGAGTTCT ATATGCCCTA CCCGGGCACC CGGATCAACC AGGAAACCGT CTCGCTCGAC | 660 |
| GCCAACGGGG TGTCTGGAAG CGCGTCGTAT TACGAAGTCA AGTTCAGCGA TCCGAGTAAG | 720 |
| CCGAACGGCC AGATCTGGAC GGGCGTAATC GGCTCGCCCG CGGCGAACGC ACCGGACGCC | 780 |
| GGGCCCCCTC AGCGCTGGTT TGTGGTATGG CTCGGGACCG CCAACAACCC GGTGGACAAG | 840 |
| GGCGCGGCCA AGGCGCTGGC CGAATCGATC CGGCCTTTGG TCGCCCCGCC GCCGGCGCCG | 900 |
| GCACCGGCTC CTGCAGAGCC CGCTCCGGCG CCGGCGCCGG CCGGGGAAGT CGCTCCTACC | 960 |
| CCGACGACAC CGACACCGCA GCGGACCTTA CCGGCCTGA | 999 |

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met His His His His His His Met His Gln Val Asp Pro Asn Leu Thr
 1 5 10 15
 Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
 20 25 30
 Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
 35 40 45
 Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
 50 55 60
 Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
 65 70 75 80
 Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
 85 90 95
 Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
 100 105 110
 Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
 115 120 125
 Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
 130 135 140
 Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
 145 150 155 160
 Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
 165 170 175
 Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
 180 185 190
 Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
 195 200 205
 Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
 210 215 220
 Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
 225 230 235 240
 Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
 245 250 255
 Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
 260 265 270
 Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
 275 280 285
 Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
 290 295 300
 Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
 305 310 315 320
 Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
 325 330

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Xaa Asn Tyr Gly Gln Val

10084843.022502

```

1           5           10           15
Val Ala Ala Leu
           20

```

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Val Glu Ser Gly Met Leu Ala Leu Gly Thr Pro Ala Pro Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala Ala Lys
1 5 10 15
Glu Gly Arg

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp Pro Ala Trp Gly Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro
 1 5 10

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Ala Ala Ala Ala Pro Pro
 1 5 10 15
 Ala

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Gln Thr Ser
 1 5 10 15

205220" 2484800T

Leu Leu Asn Asn Leu Ala Asp Pro Asp Val Ser Phe Ala Asp
 20 25 30

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Thr Gly Ser Leu Asn Gln Thr His Asn Arg Arg Ala Asn Glu Arg Lys
 1 5 10 15
 Asn Thr Thr Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala
 20 25 30
 Ala Ala Ala Ile Gly Ala Ala Ala Gly Val Thr Ser Ile Met Ala
 35 40 45
 Gly Gly Pro Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro
 50 55 60
 Leu Pro Leu Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln
 65 70 75 80
 Leu Thr Ser Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala
 85 90 95
 Asn Lys Gly Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg
 100 105 110
 Ile Ala Asp His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro
 115 120 125
 Leu Ser Phe Ser Val Thr Asn Ile Gln Pro Ala Ala Gly Ser Ala
 130 135 140
 Thr Ala Asp Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr
 145 150 155 160
 Gln Asn Val Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala
 165 170 175
 Ser Ala Met Glu Leu Leu Gln Ala Ala Gly Xaa
 180 185

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Asp Glu Val Thr Val Glu Thr Thr Ser Val Phe Arg Ala Asp Phe Leu
 1 5 10 15
 Ser Glu Leu Asp Ala Pro Ala Gln Ala Gly Thr Glu Ser Ala Val Ser
 20 25 30
 Gly Val Glu Gly Leu Pro Pro Gly Ser Ala Leu Leu Val Val Lys Arg
 35 40 45
 Gly Pro Asn Ala Gly Ser Arg Phe Leu Leu Asp Gln Ala Ile Thr Ser

205220" E4B4300T

```

      50              55              60
Ala Gly Arg His Pro Asp Ser Asp Ile Phe Leu Asp Asp Val Thr Val
65              70              75              80
Ser Arg Arg His Ala Glu Phe Arg Leu Glu Asn Asn Glu Phe Asn Val
      85              90              95
Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Val
      100             105             110
Asp Ser Ala Val Leu Ala Asn Gly Asp Glu Val Gln Ile Gly Lys Leu
      115             120             125
Arg Leu Val Phe Leu Thr Gly Pro Lys Gln Gly Glu Asp Asp Gly Ser
      130             135             140
Thr Gly Gly Pro
145

```

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

Thr Ser Asn Arg Pro Ala Arg Arg Gly Arg Arg Ala Pro Arg Asp Thr
1              5              10              15
Gly Pro Asp Arg Ser Ala Ser Leu Ser Leu Val Arg His Arg Arg Gln
      20              25              30
Gln Arg Asp Ala Leu Cys Leu Ser Thr Gln Ile Ser Arg Gln Ser
      35              40              45
Asn Leu Pro Pro Ala Ala Gly Gly Ala Ala Asn Tyr Ser Arg Arg Asn
      50              55              60
Phe Asp Val Arg Ile Lys Ile Phe Met Leu Val Thr Ala Val Val Leu
65              70              75              80
Leu Cys Cys Ser Gly Val Ala Thr Ala Ala Pro Lys Thr Tyr Cys Glu
      85              90              95
Glu Leu Lys Gly Thr Asp Thr Gly Gln Ala Cys Gln Ile Gln Met Ser
      100             105             110
Asp Pro Ala Tyr Asn Ile Asn Ile Ser Leu Pro Ser Tyr Tyr Pro Asp
      115             120             125
Gln Lys Ser Leu Glu Asn Tyr Ile Ala Gln Thr Arg Asp Lys Phe Leu
      130             135             140
Ser Ala Ala Thr Ser Ser Thr Pro Arg Glu Ala Pro Tyr Glu Leu Asn
145             150             155             160
Ile Thr Ser Ala Thr Tyr Gln Ser Ala Ile Pro Pro Arg Gly Thr Gln
      165             170             175
Ala Val Val Leu Xaa Val Tyr His Asn Ala Gly Gly Thr His Pro Thr
      180             185             190
Thr Thr Tyr Lys Ala Phe Asp Trp Asp Gln Ala Tyr Arg Lys Pro Ile
      195             200             205
Thr Tyr Asp Thr Leu Trp Gln Ala Asp Thr Asp Pro Leu Pro Val Val
      210             215             220
Phe Pro Ile Val Ala Arg
225             230

```

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1          5          10          15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20          25          30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
35          40          45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
50          55          60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65          70          75          80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85          90          95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100         105         110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
115         120         125
Gly Pro Pro Ala
130

```

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

Val Pro Leu Arg Ser Pro Ser Met Ser Pro Ser Lys Cys Leu Ala Ala
1          5          10          15
Ala Gln Arg Asn Pro Val Ile Arg Arg Arg Arg Leu Ser Asn Pro Pro
20          25          30
Pro Arg Lys Tyr Arg Ser Met Pro Ser Pro Ala Thr Ala Ser Ala Gly
35          40          45
Met Ala Arg Val Arg Arg Arg Ala Ile Trp Arg Gly Pro Ala Thr Xaa
50          55          60
Ser Ala Gly Met Ala Arg Val Arg Arg Trp Xaa Val Met Pro Xaa Val
65          70          75          80
Ile Gln Ser Thr Xaa Ile Arg Xaa Xaa Gly Pro Phe Asp Asn Arg Gly
85          90          95
Ser Glu Arg Lys
100

```

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Met Thr Asp Asp Ile Leu Leu Ile Asp Thr Asp Glu Arg Val Arg Thr
1      5      10      15
Leu Thr Leu Asn Arg Pro Gln Ser Arg Asn Ala Leu Ser Ala Ala Leu
      20      25      30
Arg Asp Arg Phe Phe Ala Xaa Leu Xaa Asp Ala Glu Xaa Asp Asp Asp
      35      40      45
Ile Asp Val Val Ile Leu Thr Gly Ala Asp Pro Val Phe Cys Ala Gly
      50      55      60
Leu Asp Leu Lys Val Ala Gly Arg Ala Asp Arg Ala Ala Gly His Leu
65      70      75      80
Thr Ala Val Gly Gly His Asp Gln Ala Gly Asp Arg Arg Asp Gln Arg
      85      90      95
Arg Arg Gly His Arg Arg Ala Arg Thr Gly Ala Val Leu Arg His Pro
      100     105     110
Asp Arg Leu Arg Ala Arg Pro Leu Arg Arg His Pro Arg Pro Gly Gly
      115     120     125
Ala Ala Ala His Leu Gly Thr Gln Cys Val Leu Ala Ala Lys Gly Arg
      130     135     140
His Arg Xaa Gly Pro Val Asp Glu Pro Asp Arg Arg Leu Pro Val Arg
145     150     155     160
Asp Arg Arg

```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

Met Lys Phe Val Asn His Ile Glu Pro Val Ala Pro Arg Arg Ala Gly
1      5      10      15
Gly Ala Val Ala Glu Val Tyr Ala Glu Ala Arg Arg Glu Phe Gly Arg
      20      25      30
Leu Pro Glu Pro Leu Ala Met Leu Ser Pro Asp Glu Gly Leu Leu Thr
      35      40      45
Ala Gly Trp Ala Thr Leu Arg Glu Thr Leu Leu Val Gly Gln Val Pro
      50      55      60
Arg Gly Arg Lys Glu Ala Val Ala Ala Val Ala Ala Ser Leu Arg
65      70      75      80
Cys Pro Trp Cys Val Asp Ala His Thr Thr Met Leu Tyr Ala Ala Gly
      85      90      95
Gln Thr Asp Thr Ala Ala Ala Ile Leu Ala Gly Thr Ala Pro Ala Ala
      100     105     110

```

Gly Asp Pro Asn Ala Pro Tyr Val Ala Trp Ala Ala Gly Thr Gly Thr
 115 120 125
 Pro Ala Gly Pro Pro Ala Pro Phe Gly Pro Asp Val Ala Ala Glu Tyr
 130 135 140
 Leu Gly Thr Ala Val Gln Phe His Phe Ile Ala Arg Leu Val Leu Val
 145 150 155 160
 Leu Leu Asp Glu Thr Phe Leu Pro Gly Gly Pro Arg Ala Gln Gln Leu
 165 170 175
 Met Arg Arg Ala Gly Gly Leu Val Phe Ala Arg Lys Val Arg Ala Glu
 180 185 190
 His Arg Pro Gly Arg Ser Thr Arg Arg Leu Glu Pro Arg Thr Leu Pro
 195 200 205
 Asp Asp Leu Ala Trp Ala Thr Pro Ser Glu Pro Ile Ala Thr Ala Phe
 210 215 220
 Ala Ala Leu Ser His His Leu Asp Thr Ala Pro His Leu Pro Pro Pro
 225 230 235 240
 Thr Arg Gln Val Val Arg Arg Val Val Gly Ser Trp His Gly Glu Pro
 245 250 255
 Met Pro Met Ser Ser Arg Trp Thr Asn Glu His Thr Ala Glu Leu Pro
 260 265 270
 Ala Asp Leu His Ala Pro Thr Arg Leu Ala Leu Leu Thr Gly Leu Ala
 275 280 285
 Pro His Gln Val Thr Asp Asp Asp Val Ala Ala Ala Arg Ser Leu Leu
 290 295 300
 Asp Thr Asp Ala Ala Leu Val Gly Ala Leu Ala Trp Ala Ala Phe Thr
 305 310 315 320
 Ala Ala Arg Arg Ile Gly Thr Trp Ile Gly Ala Ala Ala Glu Gly Gln
 325 330 335
 Val Ser Arg Gln Asn Pro Thr Gly
 340

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asp Asp Pro Asp Met Pro Gly Thr Val Ala Lys Ala Val Ala Asp Ala
 1 5 10 15
 Leu Gly Arg Gly Ile Ala Pro Val Glu Asp Ile Gln Asp Cys Val Glu
 20 25 30
 Ala Arg Leu Gly Glu Ala Gly Leu Asp Asp Val Ala Arg Val Tyr Ile
 35 40 45
 Ile Tyr Arg Gln Arg Arg Ala Glu Leu Arg Thr Ala Lys Ala Leu Leu
 50 55 60
 Gly Val Arg Asp Glu Leu Lys Leu Ser Leu Ala Ala Val Thr Val Leu
 65 70 75 80
 Arg Glu Arg Tyr Leu Leu His Asp Glu Gln Gly Arg Pro Ala Glu Ser
 85 90 95
 Thr Gly Glu Leu Met Asp Arg Ser Ala Arg Cys Val Ala Ala Ala Glu
 100 105 110

205220" E434300T

Asp Gln Tyr Glu Pro Gly Ser Ser Arg Arg Trp Ala Glu Arg Phe Ala
 115 120 125
 Thr Leu Leu Arg Asn Leu Glu Phe Leu Pro Asn Ser Pro Thr Leu Met
 130 135 140
 Asn Ser Gly Thr Asp Leu Gly Leu Leu Ala Gly Cys Phe Val Leu Pro
 145 150 155 160
 Ile Glu Asp Ser Leu Gln Ser Ile Phe Ala Thr Leu Gly Gln Ala Ala
 165 170 175
 Glu Leu Gln Arg Ala Gly Gly Gly Thr Gly Tyr Ala Phe Ser His Leu
 180 185 190
 Arg Pro Ala Gly Asp Arg Val Ala Ser Thr Gly Gly Thr Ala Ser Gly
 195 200 205
 Pro Val Ser Phe Leu Arg Leu Tyr Asp Ser Ala Ala Gly Val Val Ser
 210 215 220
 Met Gly Gly Arg Arg Arg Gly Ala Cys Met Ala Val Leu Asp Val Ser
 225 230 235 240
 His Pro Asp Ile Cys Asp Phe Val Thr Ala Lys Ala Glu Ser Pro Ser
 245 250 255
 Glu Leu Pro His Phe Asn Leu Ser Val Gly Val Thr Asp Ala Phe Leu
 260 265 270
 Arg Ala Val Glu Arg Asn Gly Leu His Arg Leu Val Asn Pro Arg Thr
 275 280 285
 Gly Lys Ile Val Ala Arg Met Pro Ala Ala Glu Leu Phe Asp Ala Ile
 290 295 300
 Cys Lys Ala Ala His Ala Gly Gly Asp Pro Gly Leu Val Phe Leu Asp
 305 310 315 320
 Thr Ile Asn Arg Ala Asn Pro Val Pro Gly Arg Gly Arg Ile Glu Ala
 325 330 335
 Thr Asn Pro Cys Gly Glu Val Pro Leu Leu Pro Tyr Glu Ser Cys Asn
 340 345 350
 Leu Gly Ser Ile Asn Leu Ala Arg Met Leu Ala Asp Gly Arg Val Asp
 355 360 365
 Trp Asp Arg Leu Glu Glu Val Ala Gly Val Ala Val Arg Phe Leu Asp
 370 375 380
 Asp Val Ile Asp Val Ser Arg Tyr Pro Phe Pro Glu Leu Gly Glu Ala
 385 390 395 400
 Ala Arg Ala Thr Arg Lys Ile Gly Leu Gly Val Met Gly Leu Ala Glu
 405 410 415
 Leu Leu Ala Ala Leu Gly Ile Pro Tyr Asp Ser Glu Glu Ala Val Arg
 420 425 430
 Leu Ala Thr Arg Leu Met Arg Arg Ile Gln Gln Ala Ala His Thr Ala
 435 440 445
 Ser Arg Arg Leu Ala Glu Glu Arg Gly Ala Phe Pro Ala Phe Thr Asp
 450 455 460
 Ser Arg Phe Ala Arg Ser Gly Pro Arg Arg Asn Ala Gln Val Thr Ser
 465 470 475 480
 Val Ala Pro Thr Gly
 485

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```

Gly Val Ile Val Leu Asp Leu Glu Pro Arg Gly Pro Leu Pro Thr Glu
1      5      10      15
Ile Tyr Trp Arg Arg Gly Leu Ala Leu Gly Ile Ala Val Val Val
20      25      30
Val Gly Ile Ala Val Ala Ile Val Ile Ala Phe Val Asp Ser Ser Ala
35      40      45
Gly Ala Lys Pro Val Ser Ala Asp Lys Pro Ala Ser Ala Gln Ser His
50      55      60
Pro Gly Ser Pro Ala Pro Gln Ala Pro Gln Pro Ala Gly Gln Thr Glu
65      70      75      80
Gly Asn Ala Ala Ala Ala Pro Pro Gln Gly Gln Asn Pro Glu Thr Pro
85      90      95
Thr Pro Thr Ala Ala Val Gln Pro Pro Pro Val Leu Lys Glu Gly Asp
100      105      110
Asp Cys Pro Asp Ser Thr Leu Ala Val Lys Gly Leu Thr Asn Ala Pro
115      120      125
Gln Tyr Tyr Val Gly Asp Gln Pro Lys Phe Thr Met Val Val Thr Asn
130      135      140
Ile Gly Leu Val Ser Cys Lys Arg Asp Val Gly Ala Ala Val Leu Ala
145      150      155      160
Ala Tyr Val Tyr Ser Leu Asp Asn Lys Arg Leu Trp Ser Asn Leu Asp
165      170      175
Cys Ala Pro Ser Asn Glu Thr Leu Val Lys Thr Phe Ser Pro Gly Glu
180      185      190
Gln Val Thr Thr Ala Val Thr Trp Thr Gly Met Gly Ser Ala Pro Arg
195      200      205
Cys Pro Leu Pro Arg Pro Ala Ile Gly Pro Gly Thr Tyr Asn Leu Val
210      215      220
Val Gln Leu Gly Asn Leu Arg Ser Leu Pro Val Pro Phe Ile Leu Asn
225      230      235      240
Gln Pro Pro Pro Pro Gly Pro Val Pro Ala Pro Gly Pro Ala Gln
245      250      255
Ala Pro Pro Pro Glu Ser Pro Ala Gln Gly Gly
260      265

```

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly Val Gln Val
1      5      10      15
Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu Val Val Ala
20      25      30
Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val Val Val Thr
35      40      45

```

2005220 "E484800T

Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu Val Ala Ala
 50 55 60
 Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr Phe Gln Asp
 65 70 75 80
 Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly Lys Ala Glu
 85 90 95
 Gln

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Gly Ala Ala Val Ser Leu Leu Ala Ala Gly Thr Leu Val Leu Thr Ala
 1 5 10 15
 Cys Gly Gly Gly Thr Asn Ser Ser Ser Ser Gly Ala Gly Gly Thr Ser
 20 25 30
 Gly Ser Val His Cys Gly Gly Lys Lys Glu Leu His Ser Ser Gly Ser
 35 40 45
 Thr Ala Gln Glu Asn Ala Met Glu Gln Phe Val Tyr Ala Tyr Val Arg
 50 55 60
 Ser Cys Pro Gly Tyr Thr Leu Asp Tyr Asn Ala Asn Gly Ser Gly Ala
 65 70 75 80
 Gly Val Thr Gln Phe Leu Asn Asn Glu Thr Asp Phe Ala Gly Ser Asp
 85 90 95
 Val Pro Leu Asn Pro Ser Thr Gly Gln Pro Asp Arg Ser Ala Glu Arg
 100 105 110
 Cys Gly Ser Pro Ala Trp Asp Leu Pro Thr Val Phe Gly Pro Ile Ala
 115 120 125
 Ile Thr Tyr Asn Ile Lys Gly Val Ser Thr Leu Asn Leu Asp Gly Pro
 130 135 140
 Thr Thr Ala Lys Ile Phe Asn Gly Thr Ile Thr Val Trp Asn Asp Pro
 145 150 155 160
 Gln Ile Gln Ala Leu Asn Ser Gly Thr Asp Leu Pro Pro Thr Pro Ile
 165 170 175
 Ser Val Ile Phe Arg Ser Asp Lys Ser Gly Thr Ser Asp Asn Phe Gln
 180 185 190
 Lys Tyr Leu Asp Gly Val Ser Asn Gly Ala Trp Gly Lys Gly Ala Ser
 195 200 205
 Glu Thr Phe Ser Gly Gly Val Gly Val Gly Ala Ser Gly Asn Asn Gly
 210 215 220
 Thr Ser Ala Leu Leu Gln Thr Thr Asp Gly Ser Ile Thr Tyr Asn Glu
 225 230 235 240
 Trp Ser Phe Ala Val Gly Lys Gln Leu Asn Met Ala Gln Ile Ile Thr
 245 250 255
 Ser Ala Gly Pro Asp Pro Val Ala Ile Thr Thr Glu Ser Val Gly Lys
 260 265 270
 Thr Ile Ala Gly Ala Lys Ile Met Gly Gln Gly Asn Asp Leu Val Leu
 275 280 285
 Asp Thr Ser Ser Phe Tyr Arg Pro Thr Gln Pro Gly Ser Tyr Pro Ile

| | | |
|---|-----|-----|
| 290 | 295 | 300 |
| Val Leu Ala Thr Tyr Glu Ile Val Cys Ser Lys Tyr Pro Asp Ala Thr | | |
| 305 | 310 | 315 |
| Thr Gly Thr Ala Val Arg Ala Phe Met Gln Ala Ala Ile Gly Pro Gly | | 320 |
| | 325 | 330 |
| Gln Glu Gly Leu Asp Gln Tyr Gly Ser Ile Pro Leu Pro Lys Ser Phe | | 335 |
| | 340 | 345 |
| Gln Ala Lys Leu Ala Ala Ala Val Asn Ala Ile Ser | | 350 |
| 355 | 360 | |

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ala | Ala | Ala | Gly | Arg | Ala | Val | Arg | Arg | Thr | Gly | His | Ala | Glu | Asp |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Gln | Thr | His | Gln | Asp | Arg | Leu | His | His | Gly | Cys | Arg | Arg | Ala | Ala | Val |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Val | Val | Arg | Gln | Asp | Arg | Ala | Ser | Val | Ser | Ala | Thr | Ser | Ala | Arg | Pro |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Pro | Arg | Arg | His | Pro | Ala | Gln | Gly | His | Arg | Arg | Arg | Val | Ala | Pro | Ser |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gly | Gly | Arg | Arg | Arg | Pro | His | Pro | His | His | Val | Gln | Pro | Asp | Asp | Arg |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Arg | Asp | Arg | Pro | Ala | Leu | Leu | Asp | Arg | Thr | Gln | Pro | Ala | Glu | His | Pro |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Asp | Pro | His | Arg | Arg | Gly | Pro | Ala | Asp | Pro | Gly | Arg | Val | Arg | Gly | Arg |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Gly | Arg | Leu | Arg | Arg | Val | Asp | Asp | Gly | Arg | Leu | Gln | Pro | Asp | Arg | Asp |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ala | Asp | His | Gly | Ala | Pro | Val | Arg | Gly | Arg | Gly | Pro | His | Arg | Gly | Val |
| | 130 | | | | | 135 | | | | 140 | | | | | |
| Gln | His | Arg | Gly | Gly | Pro | Val | Phe | Val | Arg | Arg | Val | Pro | Gly | Val | Arg |
| 145 | | | | | 150 | | | | | 155 | | | | 160 | |
| Cys | Ala | His | Arg | Arg | Gly | His | Arg | Arg | Val | Ala | Ala | Pro | Gly | Gln | Gly |
| | | | 165 | | | | | 170 | | | | | 175 | | |
| Asp | Val | Leu | Arg | Ala | Gly | Leu | Arg | Val | Glu | Arg | Leu | Arg | Pro | Val | Ala |
| | | 180 | | | | | 185 | | | | | | 190 | | |
| Ala | Val | Glu | Asn | Leu | His | Arg | Gly | Ser | Gln | Arg | Ala | Asp | Gly | Arg | Val |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Phe | Arg | Pro | Ile | Arg | Arg | Gly | Ala | Arg | Leu | Pro | Ala | Arg | Arg | Ser | Arg |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Ala | Gly | Pro | Gln | Gly | Arg | Leu | His | Leu | Asp | Gly | Ala | Gly | Pro | Ser | Pro |
| 225 | | | | | 230 | | | | | 235 | | | | 240 | |
| Leu | Pro | Ala | Arg | Ala | Gly | Gln | Gln | Gln | Pro | Ser | Ser | Ala | Gly | Gly | Arg |
| | | | 245 | | | | | 250 | | | | | 255 | | |
| Arg | Ala | Gly | Gly | Ala | Glu | Arg | Ala | Asp | Pro | Gly | Gln | Arg | Gly | Arg | His |
| | | 260 | | | | | 265 | | | | | 270 | | | |
| His | Gln | Gly | Gly | His | Asp | Pro | Gly | Arg | Gln | Gly | Ala | Gln | Arg | Gly | Thr |

275 280 285
 Ala Gly Val Ala His Ala Ala Ala Gly Pro Arg Arg Ala Ala Val Arg
 290 295 300
 Asn Arg Pro Arg Arg
 305

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ser Ala Val Trp Cys Leu Asn Gly Phe Thr Gly Arg His Arg His Gly
 1 5 10 15
 Arg Cys Arg Val Arg Ala Ser Gly Trp Arg Ser Ser Asn Arg Trp Cys
 20 25 30
 Ser Thr Thr Ala Asp Cys Cys Ala Ser Lys Thr Pro Thr Gln Ala Ala
 35 40 45
 Ser Pro Leu Glu Arg Arg Phe Thr Cys Cys Ser Pro Ala Val Gly Cys
 50 55 60
 Arg Phe Arg Ser Phe Pro Val Arg Arg Leu Ala Leu Gly Ala Arg Thr
 65 70 75 80
 Ser Arg Thr Leu Gly Val Arg Arg Thr Leu Ser Gln Trp Asn Leu Ser
 85 90 95
 Pro Arg Ala Gln Pro Ser Cys Ala Val Thr Val Glu Ser His Thr His
 100 105 110
 Ala Ser Pro Arg Met Ala Lys Leu Ala Arg Val Val Gly Leu Val Gln
 115 120 125
 Glu Glu Gln Pro Ser Asp Met Thr Asn His Pro Arg Tyr Ser Pro Pro
 130 135 140
 Pro Gln Gln Pro Gly Thr Pro Gly Tyr Ala Gln Gly Gln Gln Gln Thr
 145 150 155 160
 Tyr Ser Gln Gln Phe Asp Trp Arg Tyr Pro Pro Ser Pro Pro Pro Gln
 165 170 175
 Pro Thr Gln Tyr Arg Gln Pro Tyr Glu Ala Leu Gly Gly Thr Arg Pro
 180 185 190
 Gly Leu Ile Pro Gly Val Ile Pro Thr Met Thr Pro Pro Pro Gly Met
 195 200 205
 Val Arg Gln Arg Pro Arg Ala Gly Met Leu Ala Ile Gly Ala Val Thr
 210 215 220
 Ile Ala Val Val Ser Ala Gly Ile Gly Gly Ala Ala Ala Ser Leu Val
 225 230 235 240
 Gly Phe Asn Arg Ala Pro Ala Gly Pro Ser Gly Gly Pro Val Ala Ala
 245 250 255
 Ser Ala Ala Pro Ser Ile Pro Ala Ala Asn Met Pro Pro Gly Ser Val
 260 265 270
 Glu Gln Val Ala Ala Lys Val Val Pro Ser Val Val Met Leu Glu Thr
 275 280 285
 Asp Leu Gly Arg Gln Ser Glu Glu Gly Ser Gly Ile Ile Leu Ser Ala
 290 295 300
 Glu Gly Leu Ile Leu Thr Asn Asn His Val Ile Ala Ala Ala Ala Lys

205220 E4343001

305 310 315 320
 Pro Pro Leu Gly Ser Pro Pro Pro Lys Thr Thr Val Thr Phe Ser Asp
 325 330 335
 Gly Arg Thr Ala Pro Phe Thr Val Val Gly Ala Asp Pro Thr Ser Asp
 340 345 350
 Ile Ala Val Val Arg Val Gln Gly Val Ser Gly Leu Thr Pro Ile Ser
 355 360 365
 Leu Gly Ser Ser Ser Asp Leu Arg Val Gly Gln Pro Val Leu Ala Ile
 370 375 380
 Gly Ser Pro Leu Gly Leu Glu Gly Thr Val Thr Thr Gly Ile Val Ser
 385 390 395 400
 Ala Leu Asn Arg Pro Val Ser Thr Thr Gly Glu Ala Gly Asn Gln Asn
 405 410 415
 Thr Val Leu Asp Ala Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly Asn
 420 425 430
 Ser Gly Gly Ala Leu Val Asn Met Asn Ala Gln Leu Val Gly Val Asn
 435 440 445
 Ser Ala Ile Ala Thr Leu Gly Ala Asp Ser Ala Asp Ala Gln Ser Gly
 450 455 460
 Ser Ile Gly Leu Gly Phe Ala Ile Pro Val Asp Gln Ala Lys Arg Ile
 465 470 475 480
 Ala Asp Glu Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly
 485 490 495
 Val Gln Val Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu
 500 505 510
 Val Val Ala Gly Gly Ala Ala Asn Ala Gly Val Pro Lys Gly Val
 515 520 525
 Val Val Thr Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu
 530 535 540
 Val Ala Ala Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr
 545 550 555 560
 Phe Gln Asp Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly
 565 570 575
 Lys Ala Glu Gln
 580

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

Met Asn Asp Gly Lys Arg Ala Val Thr Ser Ala Val Leu Val Val Leu
 1 5 10 15
 Gly Ala Cys Leu Ala Leu Trp Leu Ser Gly Cys Ser Ser Pro Lys Pro
 20 25 30
 Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr Ala Ser Asp Pro
 35 40 45
 Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala Thr Lys Gly Leu
 50 55 60
 Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys Val Asp Ser Leu

(2) INFORMATION FOR SEQ ID NO:77:

(A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

[illegible]

(A) LENGTH: 69 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Pro | Ala | Pro | Pro | Leu | Pro | Pro | Leu | Pro | Pro | Ser | Pro | Ile | Ser |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

Cys Ala Ser Pro Pro Ser Pro Pro Leu Pro Pro Ala Pro Pro Val Ala
 20 25 30
 Pro Gly Pro Pro Met Pro Pro Leu Asp Pro Trp Pro Pro Ala Pro Pro
 35 40 45
 Leu Pro Tyr Ser Thr Pro Pro Gly Ala Pro Leu Pro Pro Ser Pro Pro
 50 55 60
 Ser Pro Pro Leu Pro
 65

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
 1 5 10 15
 Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
 20 25 30
 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 35 40 45
 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 50 55 60
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 65 70 75 80
 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 85 90 95
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 100 105 110
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 115 120 125
 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 130 135 140
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 145 150 155 160
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 165 170 175
 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 180 185 190
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 195 200 205
 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 210 215 220
 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
 225 230 235 240
 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
 245 250 255
 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
 260 265 270
 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
 275 280 285

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Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
 290 295 300
 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
 305 310 315 320
 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
 325 330 335
 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
 340 345 350
 Pro Pro Ala
 355

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Ser Pro Lys Pro Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr
 1 5 10 15
 Ala Ser Asp Pro Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala
 20 25 30
 Thr Lys Gly Leu Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys
 35 40 45
 Val Asp Ser Leu Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala
 50 55 60
 Asn Pro Leu Ala Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly
 65 70 75 80
 Val Pro Phe Arg Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp
 85 90 95
 Asp Trp Ser Asn Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val
 100 105 110
 Leu Asp Pro Ala Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn
 115 120 125
 Leu Gln Ala Gln Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys
 130 135 140
 Ile Thr Gly Thr Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly
 145 150 155 160
 Ala Lys Ser Ala Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser
 165 170 175
 His His Leu Val Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln
 180 185 190
 Leu Thr Gln Ser Lys Trp Asn Glu Pro Val Asn Val Asp
 195 200 205

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val
 1 5 10 15
 Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln
 20 25 30
 His Ala Asp Gly His Ser Leu Leu Asp Ala Thr Asn Pro Ala Val
 35 40 45
 Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu
 50 55 60
 Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe
 65 70 75 80
 Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu
 85 90 95
 Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala
 100 105 110
 Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val
 115 120 125
 Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp
 130 135 140
 Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn
 145 150 155 160
 Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg
 165 170 175
 Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly
 180 185 190
 Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile
 195 200 205
 Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe
 210 215 220
 Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp
 225 230 235 240
 Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg
 245 250 255
 Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln
 260 265 270
 Leu Pro Gly Phe Asp Glu Gly Gly Leu Arg Pro Xaa Lys
 275 280 285

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Thr Lys Phe His Ala Leu Met Gln Glu Gln Ile His Asn Glu Phe Thr
 1 5 10 15
 Ala Ala Gln Gln Tyr Val Ala Ile Ala Val Tyr Phe Asp Ser Glu Asp
 20 25 30
 Leu Pro Gln Leu Ala Lys His Phe Tyr Ser Gln Ala Val Glu Glu Arg

(2) INFORMATION FOR SEQ ID NO:83:

(A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ala | Asp | Glu | Arg | Lys | Asn | Thr | Thr | Met | Lys | Met | Val | Lys | Ser | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ala | Ala | Gly | Leu | Thr | Ala | Ala | Ala | Ala | Ile | Gly | Ala | Ala | Ala | Ala | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Val | Thr | Ser | Ile | Met | Ala | Gly | Gly | Pro | Val | Val | Tyr | Gln | Met | Gln | Pro |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Val | Val | Phe | Gly | Ala | Pro | Leu | Pro | Leu | Asp | Pro | Xaa | Ser | Ala | Pro | Xaa |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Val | Pro | Thr | Ala | Ala | Gln | Trp | Thr | Xaa | Leu | Leu | Asn | Xaa | Leu | Xaa | Asp |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Pro | Asn | Val | Ser | Phe | Xaa | Asn | Lys | Gly | Ser | Leu | Val | Glu | Gly | Gly | Ile |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Gly | Gly | Xaa | Glu | Gly | Xaa | Xaa | Arg | Arg | Xaa | Gln | | | | | |
| | | | 100 | | | | | 105 | | | | | | | |

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Ser | Val | Pro | Val | Gly | Asp | Gly | Phe | Trp | Xaa | Arg | Val | Val | Asn |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Pro | Leu | Gly | Gln | Pro | Ile | Asp | Gly | Arg | Gly | Asp | Val | Asp | Ser | Asp | Thr |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | | 20 | | | | | 25 | | | | 30 | | | | |
| Arg | Arg | Ala | Leu | Glu | Leu | Gln | Ala | Pro | Ser | Val | Val | Xaa | Arg | Gln | Gly |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Val | Lys | Glu | Pro | Leu | Xaa | Thr | Gly | Ile | Lys | Ala | Ile | Asp | Ala | Met | Thr |
| | | 50 | | | | | 55 | | | | | 60 | | | |
| Pro | Ile | Gly | Arg | Gly | Gln | Arg | Gln | Leu | Ile | Ile | Gly | Asp | Arg | Lys | Thr |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Gly | Lys | Asn | Arg | Arg | Leu | Cys | Arg | Thr | Pro | Ser | Ser | Asn | Gln | Arg | Glu |
| | | | 85 | | | | | | 90 | | | | 95 | | |
| Glu | Leu | Gly | Val | Arg | Trp | Ile | Pro | Arg | Ser | Arg | Cys | Ala | Cys | Val | Tyr |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Val | Gly | His | Arg | Ala | Arg | Arg | Gly | Thr | Tyr | His | Arg | Arg | | | |
| | | 115 | | | | | 120 | | | | | 125 | | | |

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Asp | Ala | Val | Met | Gly | Phe | Leu | Gly | Gly | Ala | Gly | Pro | Leu | Ala | Val |
| 1 | | | 5 | | | | | | 10 | | | | | 15 | |
| Val | Asp | Gln | Gln | Leu | Val | Thr | Arg | Val | Pro | Gln | Gly | Trp | Ser | Phe | Ala |
| | | 20 | | | | | | 25 | | | | 30 | | | |
| Gln | Ala | Ala | Ala | Val | Pro | Val | Val | Phe | Leu | Thr | Ala | Trp | Tyr | Gly | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ala | Asp | Leu | Ala | Glu | Ile | Lys | Ala | Gly | Glu | Ser | Val | Leu | Ile | His | Ala |
| | | 50 | | | | 55 | | | | 60 | | | | | |
| Gly | Thr | Gly | Gly | Val | Gly | Met | Ala | Ala | Val | Gln | Leu | Ala | Arg | Gln | Trp |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Gly | Val | Glu | Val | Phe | Val | Thr | Ala | Ser | Arg | Gly | Lys | Trp | Asp | Thr | Leu |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Arg | Ala | Xaa | Xaa | Phe | Asp | Asp | Xaa | Pro | Tyr | Arg | Xaa | Phe | Pro | His | Xaa |
| | | 100 | | | | | 105 | | | | | 110 | | | |
| Arg | Ser | Ser | Xaa | Gly | | | | | | | | | | | |
| | | 115 | | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Tyr | Arg | Phe | Ala | Cys | Arg | Thr | Leu | Met | Leu | Ala | Ala | Cys | Ile | Leu |
| 1 | | | 5 | | | | | 10 | | | | | 15 | | |
| Ala | Thr | Gly | Val | Ala | Gly | Leu | Gly | Val | Gly | Ala | Gln | Ser | Ala | Ala | Gln |
| | | 20 | | | | | 25 | | | | | 30 | | | |

```

Thr Ala Pro Val Pro Asp Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp
      35              40              45
Pro Ala Trp Gly Pro Asn Trp Asp Pro Tyr Thr Cys His Asp Asp Phe
      50              55              60
His Arg Asp Ser Asp Gly Pro Asp His Ser Arg Asp Tyr Pro Gly Pro
65              70              75              80
Ile Leu Glu Gly Pro Val Leu Asp Asp Pro Gly Ala Ala Pro Pro Pro
      85              90              95
Pro Ala Ala Gly Gly Gly Ala
      100

```

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

```

Val Gln Cys Arg Val Trp Leu Glu Ile Gln Trp Arg Gly Met Leu Gly
1              5              10              15
Ala Asp Gln Ala Arg Ala Gly Gly Pro Ala Arg Ile Trp Arg Glu His
      20              25              30
Ser Met Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala
      35              40              45
Thr Lys Glu Gly Arg Gly Ile Val Met Arg Val Pro Leu Glu Gly Gly
50              55              60
Gly Arg Leu Val Val Glu Leu Thr Pro Asp Glu Ala Ala Ala Leu Gly
65              70              75              80
Asp Glu Leu Lys Gly Val Thr Ser
      85

```

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

```

Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
1              5              10              15
Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
      20              25              30
Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
      35              40              45
Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu
50              55              60
Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
65              70              75              80
Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe

```

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85

90

95

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn
1           5           10           15
Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val
          20           25           30
Pro Ile Thr Pro Cys Glu Leu Thr Xaa Xaa Lys Asn Ala Ala Gln Gln
          35           40           45
Xaa Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
          50           55           60
Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Xaa
          65           70           75           80
Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
          85           90           95
Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
          100          105          110
Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
          115          120          125
Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
          130          135          140
Gln Gly Ala Ser Leu Ala His Xaa Gly Asp Gly Trp Asn Thr Xaa Thr
          145          150          155          160
Leu Thr Leu Gln Gly Asp
          165

```

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```

Arg Ala Glu Arg Met
1           5

```

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```

Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala
1           5           10           15
Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
20           25           30
Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
35           40           45
Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
50           55           60
Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
65           70           75           80
Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
85           90           95
Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
100          105          110
Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met
115          120          125
Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly
130          135          140
Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
145          150          155          160
His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
165          170          175
Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
180          185          190
Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr Ala
195          200          205
Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
210          215          220
Ser Ser Gly Leu Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
225          230          235          240
Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly
245          250          255
Arg Arg Asn Gly Gly Pro Ala
260

```

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```

Met Thr Tyr Ser Pro Gly Asn Pro Gly Tyr Pro Gln Ala Gln Pro Ala
1           5           10           15
Gly Ser Tyr Gly Gly Val Thr Pro Ser Phe Ala His Ala Asp Glu Gly
20           25           30
Ala Ser Lys Leu Pro Met Tyr Leu Asn Ile Ala Val Ala Val Leu Gly
35           40           45
Leu Ala Ala Tyr Phe Ala Ser Phe Gly Pro Met Phe Thr Leu Ser Thr

```

50 55 60
 Glu Leu Gly Gly Gly Asp Gly Ala Val Ser Gly Asp Thr Gly Leu Pro
 65 70 75 80
 Val Gly Val Ala Leu Leu Ala Ala Leu Leu Ala Gly Val Val Leu Val
 85 90 95
 Pro Lys Ala Lys Ser His Val Thr Val Val Ala Val Leu Gly Val Leu
 100 105 110
 Gly Val Phe Leu Met Val Ser Ala Thr Phe Asn Lys Pro Ser Ala Tyr
 115 120 125
 Ser Thr Gly Trp Ala Leu Trp Val Val Leu Ala Phe Ile Val Phe Gln
 130 135 140
 Ala Val Ala Ala Val Leu Ala Leu Leu Val Glu Thr Gly Ala Ile Thr
 145 150 155 160
 Ala Pro Ala Pro Arg Pro Lys Phe Asp Pro Tyr Gly Gln Tyr Gly Arg
 165 170 175
 Tyr Gly Gln Tyr Gly Gln Tyr Gly Val Gln Pro Gly Gly Tyr Tyr Gly
 180 185 190
 Gln Gln Gly Ala Gln Gln Ala Ala Gly Leu Gln Ser Pro Gly Pro Gln
 195 200 205
 Gln Ser Pro Gln Pro Pro Gly Tyr Gly Ser Gln Tyr Gly Gly Tyr Ser
 210 215 220
 Ser Ser Pro Ser Gln Ser Gly Ser Gly Tyr Thr Ala Gln Pro Pro Ala
 225 230 235 240
 Gln Pro Pro Ala Gln Ser Gly Ser Gln Gln Ser His Gln Gly Pro Ser
 245 250 255
 Thr Pro Pro Thr Gly Phe Pro Ser Phe Ser Pro Pro Pro Pro Val Ser
 260 265 270
 Ala Gly Thr Gly Ser Gln Ala Gly Ser Ala Pro Val Asn Tyr Ser Asn
 275 280 285
 Pro Ser Gly Gly Glu Gln Ser Ser Ser Pro Gly Gly Ala Pro Val
 290 295 300

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Gly Cys Gly Glu Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn
 1 5 10 15
 Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile
 20 25

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Gln | Val | Glu | Ser | Thr | Ala | Gly | Ser | Leu | Gln | Gly | Gln | Trp | Arg | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Cys | Gly | Ser | Thr | Ala | Gly | Ser | Leu | Gln | Gly | Gln | Trp | Arg | Gly | Ala |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ala | Gly | Thr | Ala | Ala | Gln | Ala | Ala | Val | Val | Arg | | | | | |
| | | | 20 | | | | | 25 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Cys | Gly | Gly | Thr | Ala | Ala | Gln | Ala | Ala | Val | Val | Arg | Phe | Gln | Glu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ala | Ala | Asn | Lys | Gln | Lys | Gln | Glu | Leu | Asp | Glu | | | | | |
| | | | 20 | | | | | 25 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 27 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Cys | Gly | Ala | Asn | Lys | Gln | Lys | Gln | Glu | Leu | Asp | Glu | Ile | Ser | Thr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Asn | Ile | Arg | Gln | Ala | Gly | Val | Gln | Tyr | Ser | Arg | | | | | |
| | | | 20 | | | | | 25 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 28 amino acids

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- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Gly Cys Gly Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu
 1 5 10 15
 Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
 20 25

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 507 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|-----|
| ATGAAGATGG | TGAAATCGAT | CGCCGCAGGT | CTGACCGCCG | CGGCTGCAAT | CGGCGCCGCT | 60 |
| GCGGCCGGTG | TGACTTCGAT | CATGGCTGGC | GGCCCGGTCT | TATACCAGAT | GCAGCCGGTC | 120 |
| GTCTTCGGCG | CGCCACTGCC | GTTGGACCCG | GCATCCGCCC | CTGACGTCCC | GACCGCCGCC | 180 |
| CAGTTGACCA | GCCTGCTCAA | CAGCCTCGCC | GATCCCAACG | TGTCGTTTGC | GAACAAGGGC | 240 |
| AGTCTGGTCG | AGGGCGGCAT | CGGGGGCACC | GAGGCGCGCA | TCGCCGACCA | CAAGCTGAAG | 300 |
| AAGGCCGCCG | AGCACGGGGA | TCTGCCGCTG | TCGTTTCAGCG | TGACGAACAT | CCAGCCGGCG | 360 |
| GCCGCCGGTT | CGGCCACCGC | CGACGTTTCC | GTCTCGGGTC | CGAAGCTCTC | GTCGCCGGTC | 420 |
| ACGCAGAACG | TCACGTTCTG | GAATCAAGGC | GGCTGGATGC | TGTCACGCGC | ATCGGCGGATG | 480 |
| GAGTTGCTGC | AGGCCGCAGG | GAACTGA | | | | 507 |

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala Ala Ala Ala
 1 5 10 15
 Ile Gly Ala Ala Ala Ala Gly Val Thr Ser Ile Met Ala Gly Gly Pro
 20 25 30
 Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro Leu Pro Leu
 35 40 45
 Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser
 50 55 60
 Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn Lys Gly
 65 70 75 80
 Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg Ile Ala Asp
 85 90 95
 His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro Leu Ser Phe

202502 "E4B4B43" 022502

```

          100          105          110
Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala Thr Ala Asp
          115          120          125
Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr Gln Asn Val
          130          135          140
Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala Ser Ala Met
          145          150          155          160
Glu Leu Leu Gln Ala Ala Gly Asn
          165

```

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```

CGTGGCAATG TCGTTGACCG TCGGGGCCGG GGTGCCTCC GCAGATCCCG TGGACGCGGT      60
CATTAAACACC ACCTGCAATT ACGGGCAGGT AGTAGCTGCG CTCAACGCGA CGGATCCGGG      120
GGCTGCCGCA CAGTTCAACG CCTCACCGGT GGCGCAGTCC TATTTGCGCA ATTTCTCTCGC      180
CGCACCGCCA CCTCAGCGCG CTGCCATGGC CGCGCAATTG CAAGCTGTGC CGGGGGCGGC      240
ACAGTACATC GGCCTTGTCG AGTCGGTTGC CGGCTCCTGC AACAACTATT AAGCCCATGC      300
GGGCCCCATC CCGCGACCCG GCATCGTCGC CGGGGCTAGG CCAGATTGCC CCGCTCCTCA      360
ACGGGCCGCA TCCCGCGACC CGGCATCGTC GCCGGGGCTA GGCCAGATTG CCGCGCTCCT      420
CAACGGGCCG CATCTCGTGC CGAATTCCTG CAGCCCGGGG GATCCACTAG TTCTAGAGCG      480
GCCGCCACCG CGGTGGAGCT

```

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro
1          5          10          15
Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala
          20          25          30
Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser
          35          40          45
Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
          50          55          60
Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
          65          70          75          80
Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
          85          90          95

```

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```

ATGACAGAGC AGCAGTGGAA TTTCGCGGGT ATCGAGGCCG CGGCAAGCGC AATCCAGGGA      60
AATGTCACGT CCATTCATTC CCTCCTTGAC GAGGGGAAGC AGTCCCTGAC CAAGCTCGCA      120
GCGGCCTGGG GCGGTAGCGG TTCGGAAGCG TACC                                154

```

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
1           5           10           15
Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
20           25           30
Lys Gln Ser Leu Thr Lys Leu Ala Ala Trp Gly Gly Ser Gly Ser
35           40           45
Glu Ala Tyr
50

```

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```

CGGTCGCGCA CTTCCAGGTG ACTATGAAAG TCGGCTTCCG NCTGGAGGAT TCCTGAACCT      60
TCAAGCGCGG CCGATAACTG AGGTGCATCA TTAAGCGACT TTTCCAGAAC ATCCTGACGC      120
GCTCGAAACG CGGCACAGCC GACGGTGGCT CCGNCGAGGC GCTGNCTCCA AAATCCCTGA      180
GACAATTTCG CGGGGGCGCC TACAAGGAAG TCGGTGCTGA ATTCGNCNG TATCTGGTCG      240
ACCTGTGTGG TCTGNAGCCG GACGAAGCGG TGCTCGACGT CG                                282

```

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

205220 E48B00T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

| | |
|--|------|
| GATCGTACCC GTGCGAGTGC TCGGGCCGTT TGAGGATGGA GTGCACGTGT CTTTCGTGAT | 60 |
| GGCATACCCA GAGATGTTGG CGGCGGCGGC TGACACCCTG CAGAGCATCG GTGCTACCAC | 120 |
| TGTGGCTAGC AATGCCGCTG CGGCGGCCCC GACGACTGGG GTGGTGCCCC CCGCTGCCGA | 180 |
| TGAGGTGTCG GCGCTGACTG CGGCGCACTT CGCCGCACAT GCGGCGATGT ATCAGTCCGT | 240 |
| GAGCGCTCGG GCTGCTGCGA TTCATGACCA GTTCGTGGCC ACCCTTGCCA GCAGCGCCAG | 300 |
| CTCGTATGCG GCCACTGAAG TCGCCAATGC GCGGCGGGCC AGCTAAGCCA GGAACAGTCG | 360 |
| GCACGAGAAA CCACGAGAAA TAGGGACACG TAATGGTGGA TTTCGGGGCG TTACCACCGG | 420 |
| AGATCAACTC CGCGAGGATG TACGCCGGCC CGGGTTCGGC CTCGCTGGTG GCCGCGGCTC | 480 |
| AGATGTGGGA CAGCGTGGCG AGTGACCTGT TTTCGGCCGC GTCGGCGTTT CAGTCGGTGG | 540 |
| TCTGGGGTCT GACGGTGGGG TCGTGGATAG GTTCGTCCGC GGGTCTGATG GTGGCGGCGG | 600 |
| CCTCGCCGTA TGTGGCGTGG ATGAGCGTCA CCGCGGGGCA GGCCGAGCTG ACCGCCGCC | 660 |
| AGGTCCGGGT TGCTGCGGCG GCCTACGAGA CGGCGTATGG GCTGACGGTG CCCCCGCCGG | 720 |
| TGATCGCCGA GAACCGTGCT GAACTGATGA TTCTGATAGC GACCAACCTC TTGGGGCAAA | 780 |
| ACACCCCGGC GATCGCGGTC AACGAGGCCG AATACGGCGA GATGTGGGCC CAAGACGCCG | 840 |
| CCGCGATGTT TGGCTACGCC GCGGCGACGG CGACGGCGAC GCGGACGTTG CTGCCGTTTCG | 900 |
| AGGAGGCGCC GGAGATGACC AGCGCGGGTG GGCTCCTCGA GCAGGCCGCC GCGGTCGAGG | 960 |
| AGGCCTCCGA CACCGCCGCG GCGAACCAGT TGATGAACAA TGTGCCCCAG GCGCTGCAAC | 1020 |
| AGCTGGCCCA GCCCACGCAG GGCACCACGC CTTCTTCCAA GCTGGGTGGC CTGTGGAAGA | 1080 |
| CGGTCTCGCC GCATCGGTCTG CCGATCAGCA ACATGGTGTC GATGGCCAAC AACCACATGT | 1140 |
| CGATGACCAA CTCGGGTGTG TCGATGACCA ACACCTTGAG CTCGATGTTG AAGGGCTTTG | 1200 |
| CTCCGGCGGC GGCCGCCAG GCCGTGCAAA CCGCGGCGCA AAACGGGGTC CGGGCGATGA | 1260 |
| GCTCGCTGGG CAGCTCGCTG GGTCTTTCGG GTCTGGGCGG TGGGGTGGCC GCCAACTTGG | 1320 |
| GTCGGGCGGC CTCGGTCCGT TCGTTGTCGG TGCCGCAGGC CTGGGCCGCG GCCAACCAGG | 1380 |
| CAGTCACCCC GGCGGCGCGG GCGCTGCCGC TGACCAGCCT GACCAGCGCC GCGGAAAGAG | 1440 |
| GGCCCGGGCA GATGCTGGGC GGGCTGCCGG TGGGGCAGAT GGGCGCCAGG GCCGGTGGTG | 1500 |
| GGCTCAGTGG TGTGCTGCGT GTCCGCCGC GACCCTATGT GATGCCGCAT TCTCCGGCGG | 1560 |
| CCGGCTAGGA GAGGGGGCGC AGACTGTCGT TATTTGACCA GTGATCGGCG GTCTCGGTGT | 1620 |

TTCCGCGGCC GGCTATGACA ACAGTCAATG TGCATGACAA GTTACAGGTA TTAGGTCCAG 1680
 GTTCAACAAG GAGACAGGCA ACATGGCCTC ACGTTTTATG ACGGATCCGC ACGCGATGCG 1740
 GGACATGGCG GGCCGTTTTG AGGTGCACGC CCAGACGGTG GAGGACGAGG CTCGCCGGAT 1800
 GTGGGCGTCC GCGCAAAACA TTTCCGGTGC GGGCTGGAGT GGCATGGCCG AGGCGACCTC 1860
 GCTAGACACC ATGGCCCAGA TGAATCAGGC GTTTCGCAAC ATCGTGAACA TGCTGCACGG 1920
 GGTGCGTGAC GGGCTGGTTC GCGACGCCAA CAACTACGAG CAGCAAGAGC AGGCCTCCCA 1980
 GCAGATCCTC AGCAGCTAAC GTCAGCCGCT GCAGCACAAT ACTTTTACAA GCGAAGGAGA 2040
 ACAGGTTCTGA TGACCATCAA CTATCAATTC GGGGATGTCTG ACGCTCACGG CGCCATGATC 2100
 CGCGCTCAGG CCGGGTTGCT GGAGGCCGAG CATCAGGCCA TCATTCGTGA TGTGTTGACC 2160
 GCGAGTGACT TTTGGGGCGG CGCCGGTTCG GCGGCCTGCC AGGGGTTCAT TACCCAGTTG 2220
 GGCCGTAACT TCCAGGTGAT CTACGAGCAG GCCAACGCCC ACGGGCAGAA GGTGCAGGCT 2280
 GCCGGCAACA ACATGGCGCA AACCGACAGC GCCGTCGGCT CCAGCTGGGC CTGACACCAG 2340
 GCCAAGGCCA GGGACGTGGT GTACGAGTGA AGTTCCTCGC GTGATCCTTC GGGTGGCAGT 2400
 CTAAGTGGTC AGTGCTGGGG TGTTGGTGGT TTGCTGCTTG GCGGGTTCTT CGGTGCTGGT 2460
 CAGTGCTGCT CGGGCTCGGG TGAGGACCTC GAGGCCCAGG TAGCGCCGTC CTTGATCCA 2520
 TTCGTCGTGT TGTTGCGCGA GGACGGCTCC GACGAGGCGG ATGATCGAGG CGCGGTCGGG 2580
 GAAGATGCCC ACGACGTCGG TTCGGCGTCG TACCTCTCGG TTGAGGCGTT CCTGGGGGTT 2640
 GTTGGACCAG ATTTGGCGCC AGATCTGCTT GGGGAAGGCG GTGAACGCCA GCAGGTCGGT 2700
 GCGGGCGGTG TCGAGGTGCT CGGCCACCGC GGGGAGTTTG TCGGTCAGAG CGTCGAGTAC 2760
 CCGATCATAT TGGGCAACAA CTGATTCGGC GTCGGGCTGG TCGTAGATGG AGTGCAGCAG 2820
 GGTGCGCACC CACGGCCAGG AGGGCTTCGG GGTGGCTGCC ATCAGATTGG CTGCGTAGTG 2880
 GGTTCTGCAG CGCTGCCAGG CCGCTGCGGG CAGGGTGGCG CCGATCGCGG CCACCAGGCC 2940
 GGCGTGGGCG TCGCTGGTGA CCAGCGCGAC CCCGGACAGG CCGCGGGCGA CCAGGTCGCG 3000
 GAAGAACGCC AGCCAGCCGG CCCCGTCCTC GGCGGAGGTG ACCTGGATGC CCAGGATC 3058

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Asp | Phe | Gly | Ala | Leu | Pro | Pro | Glu | Ile | Asn | Ser | Ala | Arg | Met | 1 | 5 | 10 | 15 |
| Tyr | Ala | Gly | Pro | Gly | Ser | Ala | Ser | Leu | Val | Ala | Ala | Ala | Gln | Met | Trp | 20 | 25 | 30 | |
| Asp | Ser | Val | Ala | Ser | Asp | Leu | Phe | Ser | Ala | Ala | Ser | Ala | Phe | Gln | Ser | 35 | 40 | 45 | |
| Val | Val | Trp | Gly | Leu | Thr | Val | Gly | Ser | Trp | Ile | Gly | Ser | Ser | Ala | Gly | 50 | 55 | 60 | |
| Leu | Met | Val | Ala | Ala | Ala | Ser | Pro | Tyr | Val | Ala | Trp | Met | Ser | Val | Thr | 65 | 70 | 75 | 80 |
| Ala | Gly | Gln | Ala | Glu | Leu | Thr | Ala | Ala | Gln | Val | Arg | Val | Ala | Ala | Ala | 85 | 90 | 95 | |
| Ala | Tyr | Glu | Thr | Ala | Tyr | Gly | Leu | Thr | Val | Pro | Pro | Pro | Val | Ile | Ala | 100 | 105 | 110 | |
| Glu | Asn | Arg | Ala | Glu | Leu | Met | Ile | Leu | Ile | Ala | Thr | Asn | Leu | Leu | Gly | 115 | 120 | 125 | |
| Gln | Asn | Thr | Pro | Ala | Ile | Ala | Val | Asn | Glu | Ala | Glu | Tyr | Gly | Glu | Met | 130 | 135 | 140 | |
| Trp | Ala | Gln | Asp | Ala | Ala | Ala | Met | Phe | Gly | Tyr | Ala | Ala | Ala | Thr | Ala | 145 | 150 | 155 | 160 |
| Thr | Ala | Thr | Ala | Thr | Leu | Leu | Pro | Phe | Glu | Glu | Ala | Pro | Glu | Met | Thr | 165 | 170 | 175 | |
| Ser | Ala | Gly | Gly | Leu | Leu | Glu | Gln | Ala | Ala | Ala | Val | Glu | Glu | Ala | Ser | 180 | 185 | 190 | |
| Asp | Thr | Ala | Ala | Ala | Asn | Gln | Leu | Met | Asn | Asn | Val | Pro | Gln | Ala | Leu | 195 | 200 | 205 | |
| Gln | Gln | Leu | Ala | Gln | Pro | Thr | Gln | Gly | Thr | Thr | Pro | Ser | Ser | Lys | Leu | 210 | 215 | 220 | |
| Gly | Gly | Leu | Trp | Lys | Thr | Val | Ser | Pro | His | Arg | Ser | Pro | Ile | Ser | Asn | 225 | 230 | 235 | 240 |
| Met | Val | Ser | Met | Ala | Asn | Asn | His | Met | Ser | Met | Thr | Asn | Ser | Gly | Val | 245 | 250 | 255 | |
| Ser | Met | Thr | Asn | Thr | Leu | Ser | Ser | Met | Leu | Lys | Gly | Phe | Ala | Pro | Ala | 260 | 265 | 270 | |

10084843.02200

Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
275 280 285

Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
290 295 300

Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
305 310 315 320

Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
325 330 335

Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
340 345 350

Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
355 360 365

Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
370 375 380

Pro His Ser Pro Ala Ala Gly
385 390

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

| | |
|---|-----|
| GACGTCAGCA CCCGCCGTGC AGGGCTGGAG CGTGGTCGGT TTTGATCTGC GGTCAAGGTG | 60 |
| ACGTCCCTCG GCGTGTGCGC GGCCTGGATG CAGACTCGAT GCCGCTCTTT AGTGCAACTA | 120 |
| ATTTGTTGA AGTGCCTGCG AGGTATAGGA CTTACGATT GGTAAATGTA GCGTTCACCC | 180 |
| CGTGTTGGGG TCGATTTGGC CGGACCAGTC GTCACCAACG CTTGGCGTGC GCGCCAGGCG | 240 |
| GGCGATCAGA TCGCTTGACT ACCAATCAAT CTTGAGCTCC CGGGCCGATG CTCGGGCTAA | 300 |
| ATGAGGAGGA GCACGCGTGT CTTTCACTGC GCAACCGGAG ATGTTGGCGG CCGCGGCTGG | 360 |
| CGAACTTCGT TCCCTGGGGG CAACGCTGAA GGCTAGCAAT GCCGCCGAG CCGTGCCGAC | 420 |
| GACTGGGGTG GTGCCCCGG CTGCCGACGA GGTGTCGCTG CTGCTTGCCA CACAATTCCG | 480 |
| TACGCATGCG GCGACGTATC AGACGGCCAG CGCCAAGGCC GCGGTGATCC ATGAGCAGTT | 540 |
| TGTGACCACG CTGGCCACCA GCGCTAGTTC ATATGCGGAC ACCGAGGCCG CCAACGCTGT | 600 |
| GGTCACCGGC TAGCTGACCT GACGGTATTC GAGCGGAAGG ATTATCGAAG TGGTGGATTT | 660 |

205220" E484800T

CGGGGCGTTA CCACCGGAGA TCAACTCCGC GAGGATGTAC GCCGGCCCGG GTTCGGCCTC 720
 GCTGGTGGCC GCCGCGAAGA TGTGGGACAG CGTGGCGAGT GACCTGTTTT CGGCCGCGTC 780
 GGC GTTTT CAG TCGGTGGTCT GGGGTCTGAC GGTGGGGTCG TGGATAGGTT CGTCGGCGGG 840
 TCTGATGGCG GCGGCGGCCT CGCCGTATGT GGC GTGGATG AGCGTCACCG CGGGGCAGGC 900
 CCAGCTGACC GCCGCCCAGG TCCGGGTTGC TGC GGCGGCC TACGAGACAG CGTATAGGCT 960
 GACGGTGCCC CCGCCGGTGA TCGCCGAGAA CCGTACCGAA CTGATGACGC TGACCGCGAC 1020
 CAACCTCTTG GGGCAAAACA CGCCGGCGAT CGAGGCCAAT CAGGCCGCAT ACAGCCAGAT 1080
 GTGGGGCCAA GACGCGGAGG CGATGTATGG CTACGCCGCC ACGGCGGCGA CGGCGACCGA 1140
 GGC GTTGCTG CCGTTCGAGG ACGCCCCACT GATCACCAAC CCCGGCGGGC TCCTTGAGCA 1200
 GGCCGTGCGG GTCGAGGAGG CCATCGACAC CGCCGCGGCG AACCAGTTGA TGAACAATGT 1260
 GCCCCAAGCG CTGCAACAGC TGGCCCAGCC AGCGCAGGGC GTCGTACCTT CTTCCAAGCT 1320
 GGGTGGGCTG TGGACGGCGG TCTCGCCGCA TCTGTGCGCG CTCAGCAACG TCAGTTCGAT 1380
 AGCCAACAAC CACATGTCGA TGATGGGCAC GGGTGTGTCG ATGACCAACA CCTTGCACTC 1440
 GATGTTGAAG GGCTTAGCTC CGGCGGCGGC TCAGGCCGTG GAAACCGCGG CGGAAAACGG 1500
 GGTCTGGGCG ATGAGCTCGC TGGGCAGCCA GCTGGGTTTCG TCGCTGGGTT CTTGGGTCT 1560
 GGGCGCTGGG GTGGCCGCCA ACTTGGGTCG GCGGGCTCG GTCGGTTCGT TGTCGGTGCC 1620
 GCCAGCATGG GCCGCGGCCA ACCAGGCGGT CACCCCGGCG GCGCGGGCGC TGCCGCTGAC 1680
 CAGCCTGACC AGCGCCGCCC AAACCGCCCC CGGACACATG CTGGG 1725

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1 5 10 15
 Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
 20 25 30
 Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35 40 45

Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50 55 60
 Leu Met Ala Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65 70 75 80
 Ala Gly Gln Ala Gln Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 85 90 95
 Ala Tyr Glu Thr Ala Tyr Arg Leu Thr Val Pro Pro Pro Val Ile Ala
 100 105 110
 Glu Asn Arg Thr Glu Leu Met Thr Leu Thr Ala Thr Asn Leu Leu Gly
 115 120 125
 Gln Asn Thr Pro Ala Ile Glu Ala Asn Gln Ala Ala Tyr Ser Gln Met
 130 135 140
 Trp Gly Gln Asp Ala Glu Ala Met Tyr Gly Tyr Ala Ala Thr Ala Ala
 145 150 155 160
 Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr
 165 170 175
 Asn Pro Gly Gly Leu Leu Glu Gln Ala Val Ala Val Glu Glu Ala Ile
 180 185 190
 Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
 195 200 205
 Gln Gln Leu Ala Gln Pro Ala Gln Gly Val Val Pro Ser Ser Lys Leu
 210 215 220
 Gly Gly Leu Trp Thr Ala Val Ser Pro His Leu Ser Pro Leu Ser Asn
 225 230 235 240
 Val Ser Ser Ile Ala Asn Asn His Met Ser Met Met Gly Thr Gly Val
 245 250 255
 Ser Met Thr Asn Thr Leu His Ser Met Leu Lys Gly Leu Ala Pro Ala
 260 265 270
 Ala Ala Gln Ala Val Glu Thr Ala Ala Glu Asn Gly Val Trp Ala Met
 275 280 285
 Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu
 290 295 300
 Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser
 305 310 315 320
 Leu Ser Val Pro Pro Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro
 325 330 335

2052220" E484800T
 1004848" 022202

Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr
 340 345 350

Ala Pro Gly His Met Leu Gly
 355

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

| | |
|---|------|
| AGTTCAGTCG AGAATGATAC TGACGGGCTG TATCCACGAT GGCTGAGACA ACCGAACCAC | 60 |
| CGTCGGACGC GGGGACATCG CAAGCCGACG CGATGGCGTT GGCCGCCGAA GCCGAAGCCG | 120 |
| CCGAAGCCGA AGCGCTGGCC GCCGCGGCGC GGGCCCGTGC CCGTGCCGCC CGGTTGAAGC | 180 |
| GTGAGGCGCT GGCGATGGCC CCAGCCGAGG ACGAGAACGT CCCCAGGAT ATGCAGACTG | 240 |
| GGAAGACGCC GAAGACTATG ACGACTATGA CGACTATGAG GCCGCAGACC AGGAGGCCGC | 300 |
| ACGGTCGGCA TCCTGGCGAC GGCGGTTGCG GGTGCGGTTA CCAAGACTGT CCACGATTGC | 360 |
| CATGGCGGCC GCAGTCGTCA TCATCTGCGG CTTCAACGGG CTCAGCGGAT ACATTGTGTG | 420 |
| GCAACACCAT GAGGCCACCG AACGCCAGCA GCGCGCCGCG GCGTTCGCCG CCGGAGCCAA | 480 |
| GCAAGGTGTC ATCAACATGA CCTCGCTGGA CTTCAACAAG GCCAAAGAAG ACGTCGCGCG | 540 |
| TGTGATCGAC AGCTCCACCG GCGAATTCAG GGATGACTTC CAGCAGCGGG CAGCCGATTT | 600 |
| CACCAAGGTT GTCGAACAGT CCAAAGTGGT CACCGAAGGC ACGGTGAACG CGACAGCCGT | 660 |
| CGAATCCATG AACGAGCATT CCGCCGTGGT GCTCGTCGCG GCGACTTCAC GGGTCACCAA | 720 |
| TTCCGCTGGG GCGAAAGACG AACCACGTGC GTGGCGGCTC AAAGTGACCG TGACCGAAGA | 780 |
| GGGGGGACAG TACAAGATGT CGAAAGTTGA GTTCGTACCG TGACCGATGA CGTACGCGAC | 840 |
| GTCAACACCG AAACCACTGA CGCCACCGAA GTCGCTGAGA TCGACTCAGC CGCAGGCGAA | 900 |
| GCCGGTGATT CGGCGACCGA GGCATTTGAC ACCGACTCTG CAACGGAATC TACCGCGCAG | 960 |
| AAGGGTCAGC GGCACCGTGA CCTGTGGCGA ATGCAGGTTA CTTGAAACC CGTTCCGGTG | 1020 |
| ATTCTCATCC TGCTCATGTT GATCTCTGGG GGCGCGACGG GATGGCTATA CTTGAGCAA | 1080 |
| TACGACCCGA TCAGCAGACG GACTCCGGCG CCGCCCGTGC TGCCGTCGCC GCGGCGTCTG | 1140 |
| ACGGGACAAT CGCGCTGTTG TGTATTCACC CGACACGTCG ACCAAGACTT CGCTACCGCC | 1200 |

AGGTCGCACC TCGCCGGCGA TTTCTGTCC TATACGACCA GTTCACGCAG CAGATCGTGG 1260
 CTCCGGCGGC CAAACAGAAG TCACTGAAAA CCACCGCCAA GGTGGTGCGC GCGGCCGTGT 1320
 CGGAGCTACA TCCGGATTCG GCCGTCGTTC TGGTTTTTGT CGACCAGAGC ACTACCAGTA 1380
 AGGACAGCCC CAATCCGTCG ATGGCGGCCA GCAGCGTGAT GGTGACCCTA GCCAAGGTCG 1440
 ACGGCAATTG GCTGATCACC AAGTTCACCC CGGTTTAGGT TGCCGTAGGC GGTGCGCAAG 1500
 TCTGACGGGG GCGCGGGTGG CTGCTCGTGC GAGATACCGG CCGTTCTCCG GACAATCACG 1560
 GCCCCACCTC AAACAGATCT CGGCCGCTGT CTAATCGGCC GGGTTATTTA AGATTAGTTG 1620
 CCACTGTATT TACCTGATGT TCAGATTGTT CAGCTGGATT TAGCTTCGCG GCAGGGCGGC 1680
 TGGTGCACTT TGCATCTGGG GTTGTGACTA CTTGAGAGAA TTTGACCTGT TGCCGACGTT 1740
 GTTTGCTGTC CATCATTGGT GCTAGTTATG GCCGAGCGGA AGGATTATCG AAGTGGTGGA 1800
 CTTGCGGGCG TTACCACCGG AGATCAACTC CGCGAGGATG TACGCCGGCC CGGGTTCGGC 1860
 CTCGCTGGTG GCCGCCGCGA AGATGTGGGA CAGCGTGGCG AGTGACCTGT TTTCGGCCGC 1920
 GTCGGCGTTT CAGTCGGTGG TCTGGGGTCT GACGACGGGA TCGTGGATAG GTTCGTCGGC 1980
 GGGTCTGATG GTGGCGGCGG CCTCGCCGTA TGTGGCGTGG ATGAGCGTCA CCGCGGGGCA 2040
 GGCCGAGCTG ACCGCCGCCC AGGTCCGGGT TGCTGCGGCG GCCTACGAGA CGGCGTATGG 2100
 GCTGACGGTG CCCCCGCCG TGATCGCCGA GAACCGTGCT GAACTGATGA TTCTGATAGC 2160
 GACCAACCTC TTGGGGCAAA ACACCCCGGC GATCGCGGTC AACGAGGCCG AATACGGGGA 2220
 GATGTGGGCC CAAGACGCCG CCGCGATGTT TGGCTACGCC GCCACGGCGG CGACGGCGAC 2280
 CGAGGCGTTG CTGCCGTTTC AGGACGCCCC ACTGATCACC AACCCGCGG GGCTCCTTGA 2340
 GCAGGCCGTC GCGGTCGAGG AGGCCATCGA CACCGCCGCG GCGAACCAGT TGATGAACAA 2400
 TGTGCCCCAA GCGCTGCAAC AACTGGCCCA GCCACGAAA AGCATCTGGC CGTTCGACCA 2460
 ACTGAGTGAA CTCTGGAAAG CCATCTCGCC GCATCTGTGC CCGCTCAGCA ACATCGTGTC 2520
 GATGCTCAAC AACCACGTGT CGATGACCAA CTCGGGTGTG TCGATGGCCA GCACCTTGCA 2580
 CTCAATGTTG AAGGGCTTTG CTCCGGCGGC GGCTCAGGCC GTGGAAACCG CGGCGCAAAA 2640
 CGGGGTCCAG GCGATGAGCT CGCTGGGCAG CCAGCTGGGT TCGTCGCTGG GTTCTTCGGG 2700
 TCTGGGCGCT GGGGTGGCCG CCAACTTGGG TCGGGCGGCC TCGGTCGGTT CGTTGTGGT 2760
 GCCGCAGGCC TGGGCCGCGG CCAACCAGGC GGTCAACCCG GCGGCGCGGG CGCTGCCGCT 2820

GACCAGCCTG ACCAGCGCCG CCCAAACCGC CCCC GGACAC ATGCTGGGCG GGCTACCGCT 2880
 GGGGCAACTG ACCAATAGCG GCGGCGGGTT CCGCGGGGTT AGCAATGCGT TCGCGGATGCC 2940
 GCCGCGGGCG TACGTAATGC CCCGTGTGCC CGCCGCCGGG TAACGCCGAT CCGCACGCAA 3000
 TCGGGGCCCT CTATGCGGGC AGCGATC 3027

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Asp | Phe | Gly | Ala | Leu | Pro | Pro | Glu | Ile | Asn | Ser | Ala | Arg | Met | 1 | 5 | 10 | 15 |
| Tyr | Ala | Gly | Pro | Gly | Ser | Ala | Ser | Leu | Val | Ala | Ala | Ala | Lys | Met | Trp | 20 | 25 | 30 | |
| Asp | Ser | Val | Ala | Ser | Asp | Leu | Phe | Ser | Ala | Ala | Ser | Ala | Phe | Gln | Ser | 35 | 40 | 45 | |
| Val | Val | Trp | Gly | Leu | Thr | Thr | Gly | Ser | Trp | Ile | Gly | Ser | Ser | Ala | Gly | 50 | 55 | 60 | |
| Leu | Met | Val | Ala | Ala | Ala | Ser | Pro | Tyr | Val | Ala | Trp | Met | Ser | Val | Thr | 65 | 70 | 75 | 80 |
| Ala | Gly | Gln | Ala | Glu | Leu | Thr | Ala | Ala | Gln | Val | Arg | Val | Ala | Ala | Ala | 85 | 90 | 95 | |
| Ala | Tyr | Glu | Thr | Ala | Tyr | Gly | Leu | Thr | Val | Pro | Pro | Pro | Val | Ile | Ala | 100 | 105 | 110 | |
| Glu | Asn | Arg | Ala | Glu | Leu | Met | Ile | Leu | Ile | Ala | Thr | Asn | Leu | Leu | Gly | 115 | 120 | 125 | |
| Gln | Asn | Thr | Pro | Ala | Ile | Ala | Val | Asn | Glu | Ala | Glu | Tyr | Gly | Glu | Met | 130 | 135 | 140 | |
| Trp | Ala | Gln | Asp | Ala | Ala | Ala | Met | Phe | Gly | Tyr | Ala | Ala | Thr | Ala | Ala | 145 | 150 | 155 | 160 |
| Thr | Ala | Thr | Glu | Ala | Leu | Leu | Pro | Phe | Glu | Asp | Ala | Pro | Leu | Ile | Thr | 165 | 170 | 175 | |
| Asn | Pro | Gly | Gly | Leu | Leu | Glu | Gln | Ala | Val | Ala | Val | Glu | Glu | Ala | Ile | 180 | 185 | 190 | |
| Asp | Thr | Ala | Ala | Ala | Asn | Gln | Leu | Met | Asn | Asn | Val | Pro | Gln | Ala | Leu | | | | |

| 195 | 200 | 205 |
|---|-----|-------------|
| Gln Gln Leu Ala Gln Pro Thr Lys Ser Ile Trp Pro Phe Asp Gln Leu | | |
| 210 | 215 | 220 |
| Ser Glu Leu Trp Lys Ala Ile Ser Pro His Leu Ser Pro Leu Ser Asn | | |
| 225 | 230 | 235 240 |
| Ile Val Ser Met Leu Asn Asn His Val Ser Met Thr Asn Ser Gly Val | | |
| | 245 | 250 255 |
| Ser Met Ala Ser Thr Leu His Ser Met Leu Lys Gly Phe Ala Pro Ala | | |
| | 260 | 265 270 |
| Ala Ala Gln Ala Val Glu Thr Ala Ala Gln Asn Gly Val Gln Ala Met | | |
| | 275 | 280 285 |
| Ser Ser Leu Gly Ser Gln Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu | | |
| | 290 | 295 300 |
| Gly Ala Gly Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser | | |
| | 305 | 310 315 320 |
| Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro | | |
| | 325 | 330 335 |
| Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr | | |
| | 340 | 345 350 |
| Ala Pro Gly His Met Leu Gly Gly Leu Pro Leu Gly Gln Leu Thr Asn | | |
| | 355 | 360 365 |
| Ser Gly Gly Gly Phe Gly Gly Val Ser Asn Ala Leu Arg Met Pro Pro | | |
| | 370 | 375 380 |
| Arg Ala Tyr Val Met Pro Arg Val Pro Ala Ala Gly | | |
| | 385 | 390 395 |

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

| | |
|--|-----|
| CATCGGAGGG AGTGATCACC ATGCTGTGGC ACGCAATGCC ACCGGAGTAA ATACCGCACG | 60 |
| GCTGATGGCC GGC GCGGGTC CGGCTCCAAT GCTTGCGGCG GCCGCGGGAT GGCAGACGCT | 120 |
| TTCGGCGGCT CTGGACGCTC AGGCCGTCGA GTTGACCGCG CGCCTGAACT CTCTGGGAGA | 180 |
| AGCCTGGACT GGAGGTGGCA GCGACAAGGC GCTTGCGGCT GCAACGCCGA TGGTGGTCTG | 240 |

GCTACAAACC GCGTCAACAC AGGCCAAGAC CCGTGCGATG CAGGCGACGG CGCAAGCCGC 300
 GGCATACACC CAGGCCATGG CCACGACGCC GTCGCTGCCG GAGATCGCCG CCAACCACAT 360
 CACCCAGGCC GTCCTTACGG CCACCAACTT CTTCCGGTATC AACACGATCC CGATCGCGTT 420
 GACCGAGATG GATTATTTCA TCCGTATGTG GAACCAGGCA GCCCTGGCAA TGGAGGTCTA 480
 CCAGGCCGAG ACCGCGGTTA ACACGCTTTT CGAGAAGCTC GAGCCGATGG CGTCGATCCT 540
 TGATCCCGGC GCGAGCCAGA GCACGACGAA CCCGATCTTC GGAATGCCCT CCCCTGGCAG 600
 CTCAACACCG GTTGGCCAGT TGCCGCCGGC GGCTACCCAG ACCCTCGGCC AACTGGGTGA 660
 GATGAGCGGC CCGATGCAGC AGCTGACCCA GCCGCTGCAG CAGGTGACGT CGTTGTTCAG 720
 CCAGGTGGGC GGCACCGGCG GCGGCAACCC AGCCGACGAG GAAGCCGCGC AGATGGGCCT 780
 GCTCGGCACC AGTCCGCTGT CGAACCATCC GCTGGCTGGT GGATCAGGCC CCAGCGCGGG 840
 CGCGGGCCTG CTGCGCGCGG AGTCGCTACC TGGCGCAGGT GGGTCGTTGA CCCGCACGCC 900
 GCTGATGTCT CAGCTGATCG AAAAGCCGGT TGCCCCCTCG GTGATGCCGG CGGCTGCTGC 960
 CGGATCGTCG GCGACGGGTG GCGCCGCTCC GGTGGGTGCG GGAGCGATGG GCCAGGGTGC 1020
 GCAATCCGGC GGCTCCACCA GGCCGGGTCT GGTGCGCGCG GCACCGCTCG CGCAGGAGCG 1080
 TGAAGAAGAC GACGAGGACG ACTGGGACGA AGAGGACGAC TGGTGAGCTC CCGTAATGAC 1140
 AACAGACTTC CCGGCCACCC GGGCCGGAAG ACTTGCCAAC ATTTTGGCGA GGAAGGTAAA 1200
 GAGAGAAAGT AGTCCAGCAT GGCAGAGATG AAGACCGATG CCGCTACCCT CGCGCAGGAG 1260
 GCAGGTAATT TCGAGCGGAT CTCCGGCGAC CTGAAAACCC AGATCGACCA GGTGGAGTCG 1320
 ACGGCAGGTT CGTTGCAGGG CCAGTGGCGC GGCGCGGCGG GGACGGCCGC CCAGGCCGCG 1380
 GTGGTGCGCT TCCAAGAAGC AGCCAATAAG CAGAAGCAGG AACTCGACGA GATCTCGACG 1440
 AATATTCGTC AGGCCGGCGT CCAATACTCG AGGGCCGACG AGGAGCAGCA GCAGGCGCTG 1500
 TCCTCGCAA TGGGCTTCTG ACCCGCTAAT ACGAAAAGAA ACGGAGCAAA AACATGACAG 1560
 AGCAGCAGTG GAATTTTCGCG GGTATCGAGG CCGCGGCAAG CGCAATCCAG GGAAAT 1616

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 432 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

205220 E424801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CTAGTGGATG GGACCATGGC CATTTTCTGC AGTCTCACTG CCTTCTGTGT TGACATTTTG 60
 GCACGCCGGC GGAAACGAAG CACTGGGGTC GAAGAACGGC TCGCTGCCA TATCGTCCGG 120
 AGCTTCCATA CCTTCGTGCG GCCGGAAGAG CTTGTCTAG TCGGCCGCCA TGACAACCTC 180
 TCAGAGTGCG CTCAAACGTA TAAACACGAG AAAGGGCGAG ACCGACGGAA GGTGGAACCTC 240
 GCCCATCCC GTGTTTCGCT ATTCTACGCG AACTCGGCGT TGCCCTATGC GAACATCCCA 300
 GTGACGTTGC CTTCGGTCGA AGCCATTGCC TGACCGGCTT CGCTGATCGT CCGCGCCAGG 360
 TTCTGCAGCG CGTTGTTTCTAG CTCGGTAGCC GTGGCGTCCC ATTTTGTCTG GACACCCTGG 420
 TACGCCTCCG AA 432

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met Leu Trp His Ala Met Pro Pro Glu Xaa Asn Thr Ala Arg Leu Met
 1 5 10 15
 Ala Gly Ala Gly Pro Ala Pro Met Leu Ala Ala Ala Ala Gly Trp Gln
 20 25 30
 Thr Leu Ser Ala Ala Leu Asp Ala Gln Ala Val Glu Leu Thr Ala Arg
 35 40 45
 Leu Asn Ser Leu Gly Glu Ala Trp Thr Gly Gly Gly Ser Asp Lys Ala
 50 55 60
 Leu Ala Ala Ala Thr Pro Met Val Val Trp Leu Gln Thr Ala Ser Thr
 65 70 75 80
 Gln Ala Lys Thr Arg Ala Met Gln Ala Thr Ala Gln Ala Ala Ala Tyr
 85 90 95
 Thr Gln Ala Met Ala Thr Thr Pro Ser Leu Pro Glu Ile Ala Ala Asn
 100 105 110
 His Ile Thr Gln Ala Val Leu Thr Ala Thr Asn Phe Phe Gly Ile Asn
 115 120 125
 Thr Ile Pro Ile Ala Leu Thr Glu Met Asp Tyr Phe Ile Arg Met Trp
 130 135 140

Asn Gln Ala Ala Leu Ala Met Glu Val Tyr Gln Ala Glu Thr Ala Val
 145 150 155 160
 Asn Thr Leu Phe Glu Lys Leu Glu Pro Met Ala Ser Ile Leu Asp Pro
 165 170 175
 Gly Ala Ser Gln Ser Thr Thr Asn Pro Ile Phe Gly Met Pro Ser Pro
 180 185 190
 Gly Ser Ser Thr Pro Val Gly Gln Leu Pro Pro Ala Ala Thr Gln Thr
 195 200 205
 Leu Gly Gln Leu Gly Glu Met Ser Gly Pro Met Gln Gln Leu Thr Gln
 210 215 220
 Pro Leu Gln Gln Val Thr Ser Leu Phe Ser Gln Val Gly Gly Thr Gly
 225 230 235 240
 Gly Gly Asn Pro Ala Asp Glu Glu Ala Ala Gln Met Gly Leu Leu Gly
 245 250 255
 Thr Ser Pro Leu Ser Asn His Pro Leu Ala Gly Gly Ser Gly Pro Ser
 260 265 270
 Ala Gly Ala Gly Leu Leu Arg Ala Glu Ser Leu Pro Gly Ala Gly Gly
 275 280 285
 Ser Leu Thr Arg Thr Pro Leu Met Ser Gln Leu Ile Glu Lys Pro Val
 290 295 300
 Ala Pro Ser Val Met Pro Ala Ala Ala Ala Gly Ser Ser Ala Thr Gly
 305 310 315 320
 Gly Ala Ala Pro Val Gly Ala Gly Ala Met Gly Gln Gly Ala Gln Ser
 325 330 335
 Gly Gly Ser Thr Arg Pro Gly Leu Val Ala Pro Ala Pro Leu Ala Gln
 340 345 350
 Glu Arg Glu Glu Asp Asp Glu Asp Asp Trp Asp Glu Glu Asp Asp Trp
 355 360 365

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

Met Ala Glu Met Lys Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly
 1 5 10 15

Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val
 20 25 30
 Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly
 35 40 45
 Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys
 50 55 60
 Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly
 65 70 75 80
 Val Gln Tyr Ser Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser
 85 90 95
 Gln Met Gly Phe
 100

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

| | |
|--|-----|
| GATCTCCGGC GACCTGAAAA CCCAGATCGA CCAGGTGGAG TCGACGGCAG GTTCGTTGCA | 60 |
| GGGCCAGTGG CGCGGCGCGG CGGGGACGGC CGCCAGGCC GCGGTGGTGC GCTTCCAAGA | 120 |
| AGCAGCCAAT AAGCAGAAGC AGGAACTCGA CGAGATCTCG ACGAATATTC GTCAGGCCCGG | 180 |
| CGTCCAATAC TCGAGGGCCG ACGAGGAGCA GCAGCAGGCG CTGTCCTCGC AAATGGGCTT | 240 |
| CTGACCCGCT AATACGAAAA GAAACGGAGC AAAAACATGA CAGAGCAGCA GTGGAATTTC | 300 |
| GCGGGTATCG AGGCCGCGGC AAGCGCAATC CAGGGAAATG TCACGTCCAT TCATTCCCTC | 360 |
| CTTGACGAGG GGAAGCAGTC CCTGACCAAG CTCGCA | 396 |

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

| |
|--|
| Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala |
| 1 5 10 15 |

Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln
 20 25 30

Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu
 35 40 45

Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser
 50 55 60

Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
 65 70 75 80

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GTGGATCCCG ATCCCGTGTT TCGCTATTCT ACGCGAACTC GGCGTTGCCC TATGCGAACA 60

TCCCAGTGAC GTTGCCCTTCG GTCGAAGCCA TTGCCTGACC GGCTTCGCTG ATCGTCCGCG 120

CCAGGTTCTG CAGCGCGTTG TTCAGCTCGG TAGCCGTGGC GTCCCATTTT TGCTGGACAC 180

CCTGGTACGC CTCCGAACCG CTACCGCCCC AGGCCGCTGC GAGCTTGGTC AGGGACTGCT 240

TCCCCTCGTC AAGGAGGGAA TGAATGGACG TGACATTTCC CTGGATTGCG CTTGCCGCGG 300

CCTCGATACC CGCGAAATTC CACTGCTGCT CTGTCATGTT TTTGCTCCGT TTCTTTTCGT 360

ATTAGCGGGT CAGAAGCCCA TTGCGA 387

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CGGCACGAGG ATCTCGGTTG GCCCAACGGC GCTGGCGAGG GCTCCGTTCC GGGGGCGAGC 60

TGCGCGCCGG ATGCTTCCTC TGCCCGCAGC CGCGCCTGGA TGGATGGACC AGTTGCTACC 120

TTCCCGACGT TTCGTTCCGT GTCTGTGCGA TAGCGGTGAC CCCGGCGCGC ACGTCGGGAG 180

TGTTGGGGGG CAGGCCGGGT CGGTGGTTCG GCCGGGGACG CAGACGGTCT GGACGGAACG 240

272

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Ala Val Glu Ser Gly Met Leu Ala Leu Gly Thr Pro Ala Pro Ser
1 5 10 15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala Ala Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp Pro Ala Trp Gly Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro
1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser
1 5 10 15

Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn
20 25 30

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Asp Pro Pro Asp Pro His Gln Xaa Asp Met Thr Lys Gly Tyr Tyr Pro
1 5 10 15

Gly Gly Arg Arg Xaa Phe
20

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Pro Gly Tyr Thr Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Second Residue Can Be Either a Pro or Thr"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

Xaa Xaa Gly Phe Thr Gly Pro Gln Phe Tyr
 1 5 10

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: /note= "The Third Residue Can Be Either a Gln or Leu"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

Xaa Pro Xaa Val Thr Ala Tyr Ala Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

Xaa Xaa Xaa Glu Lys Pro Phe Leu Arg
 1 5

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

Xaa Asp Ser Glu Lys Ser Ala Thr Ile Lys Val Thr Asp Ala Ser
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gly | Asp | Thr | Xaa | Ile | Tyr | Ile | Val | Gly | Asn | Leu | Thr | Ala | Asp |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |

(2) INFORMATION FOR SEQ ID NO:136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Glu | Ser | Gly | Ala | Gly | Leu | Gly | Gly | Thr | Val | Gln | Ala | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 |

(2) INFORMATION FOR SEQ ID NO:137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Xaa | Tyr | Ile | Ala | Tyr | Xaa | Thr | Thr | Ala | Gly | Ile | Val | Pro | Gly | Lys | Ile |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

| | | | | |
|-----|-----|-----|-----|-----|
| Asn | Val | His | Leu | Val |
| | | | 20 | |

(2) INFORMATION FOR SEQ ID NO:138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 882 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GCAACGCTGT CGTGGCCTTT GCGGTGATCG GTTTCGCCTC GCTGGCGGTG GCGGTGGCGG 60
 TCACCATCCG ACCGACCGCG GCCTCAAAAC CGGTAGAGGG ACACCAAAC GCCCAGCCAG 120
 GGAAGTTCAT GCCGTTGTTG CCGACGCAAC AGCAGGCGCC GGTCCCGCCG CCTCCGCCCG 180
 ATGATCCCAC CGCTGGATT CAGGGCGGCA CCATTCCGGC TGTACAGAAC GTGGTGCCGC 240
 GGCCGGGTAC CTCACCCGGG GTGGGTGGGA CGCCGGCTTC GCCTGCGCCG GAAGCGCCGG 300
 CCGTGCCCGG TGTTGTGCCT GCCCCGGTGC CAATCCCGGT CCCGATCATC ATTCCCCCGT 360
 TCCCGGGTTG GCAGCCTGGA ATGCCGACCA TCCCACCGC ACCGCCGACG ACGCCGGTGA 420
 CCACGTCGGC GACGACGCCG CCGACCACGC CGCCGACCAC GCCGGTGACC ACGCCGCCAA 480
 CGACGCCGCC GACCACGCCG GTGACCACGC CGCCAACGAC GCCGCCGACC ACGCCGGTGA 540
 CCACGCCACC AACGACCGTC GCCCCGACGA CCGTCGCCCC GACGACGGTC GCTCCGACCA 600
 CCGTCGCCCC GACCACGGTC GCTCCAGCCA CCGCCACGCC GACGACCGTC GCTCCGCAGC 660
 CGACGCAGCA GCCCAGCAA CAACCAACCC AACAGATGCC AACCAGCAG CAGACCGTGG 720
 CCCCAGAC GGTGGCGCCG GCTCCGCAGC CGCCGTCCGG TGGCCGAAC GGCAGCGGCG 780
 GGGGCGACTT ATTCGGCGGG TTCTGATCAC GGTCGCGGCT TCACTACGGT CGGAGGACAT 840
 GGCCGGTGAT GCGGTGACGG TGGTGCTGCC CTGTCTCAAC GA 882

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 815 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CCATCAACCA ACCGCTCGCG CCGCCCGCGC CGCCGGATCC GCCGTCGCCG CCACGCCCGC 60
 CCGTGCCCTCC GGTGCCCCCG TTGCCGCCGT CGCCGCCGTC GCCGCCGACC GGCTGGGTGC 120
 CTAGGGCGCT GTTACCGCCC TGGTTGGCGG GGACGCCGCC GGCACCACCG GTACCGCCGA 180
 TGGCGCCGTT GCCGCCGGCG GCACCGTTGC CACCGTTGCC ACCGTTGCCA CCGTTGCCGA 240
 CCAGCCACCC GCCGCGACCA CCGGCACCGC CGGCGCCGCC CGCACCGCCG GCGTGCCCGT 300
 TCGTGCCCGT ACCGCCGGCA CCGCCGTTGC CGCCGTCACC GCCGACGGAA CTACCGGCGG 360
 ACGCGGCCTG CCCGCCGGCG CCGCCCGCAC CGCCATTGGC ACCGCCGTCA CCGCCGGCTG 420

GGAGTGCCGC GATTAGGGCA CTGACCGGCG CAACCAGCGC AAGTACTCTC GGTCACCGAG 480
 CACTTCCAGA CGACACCACA GCACGGGGTT GTCGGCGGAC TGGGTGAAAT GGCAGCCGAT 540
 AGCGGCTAGC TGTCGGCTGC GGTCAACCTC GATCATGATG TCGAGGTGAC CGTGACCGCG 600
 CCCCCGAAG GAGGCGCTGA ACTCGGCGTT GAGCCGATCG GCGATCGGTT GGGGCAGTGC 660
 CCAGGCCAAT ACGGGGATAC CGGGTGTGNA AGCCGCCGCG AGCGCAGCTT CGGTTGCGCG 720
 ACNGTGGTCG GGGTGGCCTG TTACGCCGTT GTCNTCGAAC ACGAGTAGCA GGTCTGCTCC 780
 GGCGAGGGCA TCCACCACGC GTTGCCTCAG CTCGT 815

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1152 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAGCCGCC GGCTGAGGTC TCAGATCAGA GAGTCTCCGG ACTCACCGGG GCGGTTTCAGC 60
 CTTCTCCCAG AACAACTGCT GAAGATCCTC GCGCGGAAA CAGGCGCTGA TTTGACGCTC 120
 TATGACCGGT TGAACGACGA GATCATCCGG CAGATTGATA TGGCACCGCT GGGCTAACAG 180
 GTGCGCAAGA TGGTGCAGCT GTATGTCTCG GACTCCGTGT CGCGGATCAG CTTTGCCGAC 240
 GGCCGGGTGA TCGTGTGGAG CGAGGAGCTC GGCGAGAGCC AGTATCCGAT CGAGACGCTG 300
 GACGGCATCA CGCTGTTTGG GCGGCCGACG ATGACAACGC CCTTCATCGT TGAGATGCTC 360
 AAGCGTGAGC GCGACATCCA GCTCTTCACG ACCGACGGCC ACTACCAGGG CCGGATCTCA 420
 ACACCCGACG TGTCATACGC GCCGCGGCTC CGTCAGCAAG TTCACCGCAC CGACGATCCT 480
 GCGTTCTGCC TGTCGTTAAG CAAGCGGATC GTGTCGAGGA AGATCCTGAA TCAGCAGGCC 540
 TTGATTCGGG CACACACGTC GGGGCAAGAC GTTGCTGAGA GCATCCGCAC GATGAAGCAC 600
 TCGCTGGCCT GGGTCGATCG ATCGGGCTCC CTGGCGGAGT TGAACGGGTT CGAGGGAAAT 660
 GCCGCAAAGG CATACTTCAC CGCGCTGGGG CATCTCGTCC CGCAGGAGTT CGCATTCAG 720
 GGCCGCTCGA CTCGGCCGCC GTTGGACGCC TTCAACTCGA TGGTCAGCCT CGGCTATTCG 780
 CTGCTGTACA AGAACATCAT AGGGGCGATC GAGCGTCACA GCCTGAACGC GTATATCGGT 840

TTCCTACACC AGGATTACAG AGGGCACGCA ACGTCTCGTG CCGAATTCGG CACGAGCTCC 900
 GCTGAAACCG CTGGCCGGCT GCTCAGTGCC CGTACGTAAT CCGCTGCGCC CAGGCCGGCC 960
 CGCCGGCCGA ATACCAGCAG ATCGGACAGC GAATTGCCGC CCAGCCGGTT GGAGCCGTGC 1020
 ATACCGCCGG CACACTCACC GGCAGCGAAC AGGCCTGGCA CCGTGGCGGC GCCGGTGTCC 1080
 GCGTCTACTT CGACACCGCC CATCACGTAG TGACACGTCG GCCCGACTTC CATTGCCTGC 1140
 GTTCGGCACG AG 1152

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 655 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

CTCGTGCCGA TTCGGCAGGG TGTACTTGCC GGTGGTGTAN GCCGCATGAG TGCCGACGAC 60
 CAGCAATGCG GCAACAGCAC GGATCCCGGT CAACGACGCC ACCCGGTCCA CGTGGGCGAT 120
 CCGCTCGAGT CCGCCCTGGG CGGCTCTTTC CTTGGGCAGG GTCATCCGAC GTGTTTCCGC 180
 CGTGGTTTGC CGCCATTATG CCGGCGCGCC GCGTCGGGCG GCCGGTATGG CCGAANGTCG 240
 ATCAGCACAC CCGAGATACG GGTCTGTGCA AGCTTTTGA GCGTCGCGCG GGGCAGCTTC 300
 GCCGGCAATT CTACTAGCGA GAAGTCTGGC CCGATACGGA TCTGACCGAA GTCGCTGCGG 360
 TGCAGCCCAC CCTCATTGGC GATGGCGCCG ACGATGGCGC CTGGACCGAT CTTGTGCCGC 420
 TTGCCGACGG CGACGCGGTA GGTGGTCAAG TCCGGTCTAC GCTTGGGCCT TTGCGGACGG 480
 TCCCGACGCT GGTGCGGGTT GCGCCGCGAA AGCGGCGGGT CGGGTGCCAT CAGGAATGCC 540
 TCACCGCCGC GGCAGTGCAC GGCCAGTGCC GCGGCGATGT CAGCCATCGG GACATCATGC 600
 TCGCGTTCAT ACTCCTCGAC CAGTCGGCGG AACAGCTCGA TTCCCGGACC GCCCA 655

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

20220420 14:43:07

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Asn Ala Val Val Ala Phe Ala Val Ile Gly Phe Ala Ser Leu Ala Val
 1 5 10 15
 Ala Val Ala Val Thr Ile Arg Pro Thr Ala Ala Ser Lys Pro Val Glu
 20 25 30
 Gly His Gln Asn Ala Gln Pro Gly Lys Phe Met Pro Leu Leu Pro Thr
 35 40 45
 Gln Gln Gln Ala Pro Val Pro Pro Pro Pro Pro Asp Asp Pro Thr Ala
 50 55 60
 Gly Phe Gln Gly Gly Thr Ile Pro Ala Val Gln Asn Val Val Pro Arg
 65 70 75 80
 Pro Gly Thr Ser Pro Gly Val Gly Gly Thr Pro Ala Ser Pro Ala Pro
 85 90 95
 Glu Ala Pro Ala Val Pro Gly Val Val Pro Ala Pro Val Pro Ile Pro
 100 105 110
 Val Pro Ile Ile Ile Pro Pro Phe Pro Gly Trp Gln Pro Gly Met Pro
 115 120 125
 Thr Ile Pro Thr Ala Pro Pro Thr Thr Pro Val Thr Thr Ser Ala Thr
 130 135 140
 Thr Pro Pro Thr Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr
 145 150 155 160
 Thr Pro Pro Thr Thr Pro Val Thr Thr Pro Pro Thr Thr Pro Pro Thr
 165 170 175
 Thr Pro Val Thr Thr Pro Pro Thr Thr Val Ala Pro Thr Thr Val Ala
 180 185 190
 Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro Thr Thr Val Ala Pro
 195 200 205
 Ala Thr Ala Thr Pro Thr Thr Val Ala Pro Gln Pro Thr Gln Gln Pro
 210 215 220
 Thr Gln Gln Pro Thr Gln Gln Met Pro Thr Gln Gln Gln Thr Val Ala
 225 230 235 240
 Pro Gln Thr Val Ala Pro Ala Pro Gln Pro Pro Ser Gly Gly Arg Asn
 245 250 255
 Gly Ser Gly Gly Gly Asp Leu Phe Gly Gly Phe
 260 265

(2) INFORMATION FOR SEQ ID NO:143:

205220" E494B00F

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Asn | Gln | Pro | Leu | Ala | Pro | Pro | Ala | Pro | Pro | Asp | Pro | Pro | Ser | Pro | 1 | 5 | 10 | 15 |
| Pro | Arg | Pro | Pro | Val | Pro | Pro | Val | Pro | Pro | Leu | Pro | Pro | Ser | Pro | Pro | 20 | 25 | 30 | |
| Ser | Pro | Pro | Thr | Gly | Trp | Val | Pro | Arg | Ala | Leu | Leu | Pro | Pro | Trp | Leu | 35 | 40 | 45 | |
| Ala | Gly | Thr | Pro | Pro | Ala | Pro | Pro | Val | Pro | Pro | Met | Ala | Pro | Leu | Pro | 50 | 55 | 60 | |
| Pro | Ala | Ala | Pro | Leu | Pro | Pro | Leu | Pro | Pro | Leu | Pro | Pro | Leu | Pro | Thr | 65 | 70 | 75 | 80 |
| Ser | His | Pro | Pro | Arg | Pro | Pro | Ala | Pro | Pro | Ala | Pro | Pro | Ala | Pro | Pro | 85 | 90 | 95 | |
| Ala | Cys | Pro | Phe | Val | Pro | Val | Pro | Pro | Ala | Pro | Pro | Leu | Pro | Pro | Ser | 100 | 105 | 110 | |
| Pro | Pro | Thr | Glu | Leu | Pro | Ala | Asp | Ala | Ala | Cys | Pro | Pro | Ala | Pro | Pro | 115 | 120 | 125 | |
| Ala | Pro | Pro | Leu | Ala | Pro | Pro | Ser | Pro | Pro | Ala | Gly | Ser | Ala | Ala | Ile | 130 | 135 | 140 | |
| Arg | Ala | Leu | Thr | Gly | Ala | Thr | Ser | Ala | Ser | Thr | Leu | Gly | His | Arg | Ala | 145 | 150 | 155 | 160 |
| Leu | Pro | Asp | Asp | Thr | Thr | Ala | Arg | Gly | Cys | Arg | Arg | Thr | Gly | | | 165 | 170 | | |

(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

Gln Pro Pro Ala Glu Val Ser Asp Gln Arg Val Ser Gly Leu Thr Gly
 1 5 10 15
 Ala Val Gln Pro Ser Pro Arg Thr Thr Ala Glu Asp Pro Arg Pro Arg
 20 25 30
 Asn Arg Arg
 35

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Arg Ala Asp Ser Ala Gly Cys Thr Cys Arg Trp Cys Xaa Pro His Glu
 1 5 10 15
 Cys Arg Arg Pro Ala Met Arg Gln Gln His Gly Ser Arg Ser Thr Thr
 20 25 30
 Pro Pro Gly Pro Arg Gly Arg Ser Ala Arg Val Arg Pro Gly Arg Leu
 35 40 45
 Phe Pro Trp Ala Gly Ser Ser Asp Val Phe Pro Pro Trp Phe Ala Ala
 50 55 60
 Ile Met Pro Ala Arg Arg Val Gly Arg Pro Val Trp Pro Xaa Val Asp
 65 70 75 80
 Gln His Thr Arg Asp Thr Gly Leu Cys Lys Leu Phe Glu Arg Arg Ala
 85 90 95
 Gly Gln Leu Arg Arg Gln Phe Tyr
 100

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGATCGA CATCATCGGG ACC

53

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CCTGAATTCA GGCCTCGGTT GCGCCGGCCT CATCTTGAAC GA

42

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GGATCCTGCA GGCTCGAAAC CACCGAGCGG T

31

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

1002441.03502

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CTCTGAATTC AGCGCTGGAA ATCGTCGCGA T

31

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GGATCCAGCG CTGAGATGAA GACCGATGCC GCT

33

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GAGAGAATTC TCAGAAGCCC ATTTGCGAGG ACA

33

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(ix) FEATURE:

10044344 03200

(A) NAME/KEY: CDS

(B) LOCATION: 152..1273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

| | |
|---|-----|
| TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCCACCGA ACAGCTGTTG TCCTCGCCGA | 60 |
| AGCATGCGGA AACCGCCCGA TACGTCGCCG GACTGTCGGG GGACGTCAAG GACGCCAAGC | 120 |
| GCGGAAATTG AAGAGCACAG AAAGGTATGG C GTG AAA ATT CGT TTG CAT ACG | 172 |
| Val Lys Ile Arg Leu His Thr | |
| 1 5 | |
| CTG TTG GCC GTG TTG ACC GCT GCG CCG CTG CTG CTA GCA GCG GCG GGC | 220 |
| Leu Leu Ala Val Leu Thr Ala Ala Pro Leu Leu Leu Ala Ala Ala Gly | |
| 10 15 20 | |
| TGT GGC TCG AAA CCA CCG AGC GGT TCG CCT GAA ACG GGC GCC GGC GCC | 268 |
| Cys Gly Ser Lys Pro Pro Ser Gly Ser Pro Glu Thr Gly Ala Gly Ala | |
| 25 30 35 | |
| GGT ACT GTC GCG ACT ACC CCC GCG TCG TCG CCG GTG ACG TTG GCG GAG | 316 |
| Gly Thr Val Ala Thr Thr Pro Ala Ser Ser Pro Val Thr Leu Ala Glu | |
| 40 45 50 55 | |
| ACC GGT AGC ACG CTG CTC TAC CCG CTG TTC AAC CTG TGG GGT CCG GCC | 364 |
| Thr Gly Ser Thr Leu Leu Tyr Pro Leu Phe Asn Leu Trp Gly Pro Ala | |
| 60 65 70 | |
| TTT CAC GAG AGG TAT CCG AAC GTC ACG ATC ACC GCT CAG GGC ACC GGT | 412 |
| Phe His Glu Arg Tyr Pro Asn Val Thr Ile Thr Ala Gln Gly Thr Gly | |
| 75 80 85 | |
| TCT GGT GCC GGG ATC GCG CAG GCC GCC GCC GGG ACG GTC AAC ATT GGG | 460 |
| Ser Gly Ala Gly Ile Ala Gln Ala Ala Ala Gly Thr Val Asn Ile Gly | |
| 90 95 100 | |
| GCC TCC GAC GCC TAT CTG TCG GAA GGT GAT ATG GCC GCG CAC AAG GGG | 508 |
| Ala Ser Asp Ala Tyr Leu Ser Glu Gly Asp Met Ala Ala His Lys Gly | |
| 105 110 115 | |
| CTG ATG AAC ATC GCG CTA GCC ATC TCC GCT CAG CAG GTC AAC TAC AAC | 556 |
| Leu Met Asn Ile Ala Leu Ala Ile Ser Ala Gln Gln Val Asn Tyr Asn | |
| 120 125 130 135 | |
| CTG CCC GGA GTG AGC GAG CAC CTC AAG CTG AAC GGA AAA GTC CTG GCG | 604 |
| Leu Pro Gly Val Ser Glu His Leu Lys Leu Asn Gly Lys Val Leu Ala | |
| 140 145 150 | |
| GCC ATG TAC CAG GGC ACC ATC AAA ACC TGG GAC GAC CCG CAG ATC GCT | 652 |
| Ala Met Tyr Gln Gly Thr Ile Lys Thr Trp Asp Asp Pro Gln Ile Ala | |
| 155 160 165 | |
| GCG CTC AAC CCC GGC GTG AAC CTG CCC GGC ACC GCG GTA GTT CCG CTG | 700 |
| Ala Leu Asn Pro Gly Val Asn Leu Pro Gly Thr Ala Val Val Pro Leu | |

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| 170 | 175 | 180 | |
|---|-----|-----|------|
| CAC CGC TCC GAC GGG TCC GGT GAC ACC TTC TTG TTC ACC CAG TAC CTG His Arg Ser Asp Gly Ser Gly Asp Thr Phe Leu Phe Thr Gln Tyr Leu 185 190 195 | | | 748 |
| TCC AAG CAA GAT CCC GAG GGC TGG GGC AAG TCG CCC GGC TTC GGC ACC Ser Lys Gln Asp Pro Glu Gly Trp Gly Lys Ser Pro Gly Phe Gly Thr 200 205 210 215 | | | 796 |
| ACC GTC GAC TTC CCG GCG GTG CCG GGT GCG CTG GGT GAG AAC GGC AAC Thr Val Asp Phe Pro Ala Val Pro Gly Ala Leu Gly Glu Asn Gly Asn 220 225 230 | | | 844 |
| GGC GGC ATG GTG ACC GGT TGC GCC GAG ACA CCG GGC TGC GTG GCC TAT Gly Gly Met Val Thr Gly Cys Ala Glu Thr Pro Gly Cys Val Ala Tyr 235 240 245 | | | 892 |
| ATC GGC ATC AGC TTC CTC GAC CAG GCC AGT CAA CGG GGA CTC GGC GAG Ile Gly Ile Ser Phe Leu Asp Gln Ala Ser Gln Arg Gly Leu Gly Glu 250 255 260 | | | 940 |
| GCC CAA CTA GGC AAT AGC TCT GGC AAT TTC TTG TTG CCC GAC GCG CAA Ala Gln Leu Gly Asn Ser Ser Gly Asn Phe Leu Leu Pro Asp Ala Gln 265 270 275 | | | 988 |
| AGC ATT CAG GCC GCG GCG GCT GGC TTC GCA TCG AAA ACC CCG GCG AAC Ser Ile Gln Ala Ala Ala Ala Gly Phe Ala Ser Lys Thr Pro Ala Asn 280 285 290 295 | | | 1036 |
| CAG GCG ATT TCG ATG ATC GAC GGG CCC GCC CCG GAC GGC TAC CCG ATC Gln Ala Ile Ser Met Ile Asp Gly Pro Ala Pro Asp Gly Tyr Pro Ile 300 305 310 | | | 1084 |
| ATC AAC TAC GAG TAC GCC ATC GTC AAC AAC CGG CAA AAG GAC GCC GCC Ile Asn Tyr Glu Tyr Ala Ile Val Asn Asn Arg Gln Lys Asp Ala Ala 315 320 325 | | | 1132 |
| ACC GCG CAG ACC TTG CAG GCA TTT CTG CAC TGG GCG ATC ACC GAC GGC Thr Ala Gln Thr Leu Gln Ala Phe Leu His Trp Ala Ile Thr Asp Gly 330 335 340 | | | 1180 |
| AAC AAG GCC TCG TTC CTC GAC CAG GTT CAT TTC CAG CCG CTG CCG CCC Asn Lys Ala Ser Phe Leu Asp Gln Val His Phe Gln Pro Leu Pro Pro 345 350 355 | | | 1228 |
| GCG GTG GTG AAG TTG TCT GAC GCG TTG ATC GCG ACG ATT TCC AGC Ala Val Val Lys Leu Ser Asp Ala Leu Ile Ala Thr Ile Ser Ser 360 365 370 | | | 1273 |
| TAGCCTCGTT GACCACCACG CGACAGCAAC CTCCGTCGGG CCATCGGGCT GCTTTGCGGA | | | 1333 |
| GCATGCTGGC CCGTGCCGGT GAAGTCGGCC GCGCTGGCCC GGCCATCCGG TGGTTGGGTG | | | 1393 |
| GGATAGGTGC GGTGATCCCG CTGCTTGCGC TGGTCTTGGT GCTGGTGGTG CTGGTCATCG | | | 1453 |

2025-02-20 10:44:43

AGGCGATGGG TGCATCAGG CTCAACGGGT TGCATTTCTT CACCGCCACC GAATGGAATC 1513
 CAGGCAACAC CTACGGCGAA ACCGTTGTCA CCGACGCGTC GCCCATCCGG TCGGCGCCTA 1573
 CTACGGGGCG TTGCCGCTGA TCGTCGGGAC GCTGGCGACC TCGGCAATCG CCCTGATCAT 1633
 CGCGGTGCCG GTCTCTGTAG GAGCGGCGCT GGTGATCGTG GAACGGCTGC CGAAACGGTT 1693
 GGCCGAGGCT GTGGGAATAG TCCTGGAATT GCTCGCCGGA ATCCCAGCG TGGTCGTCGG 1753
 TTTGTGGGGG GCAATGACGT TCGGGCCGTT CATCGCTCAT CACATCGCTC CGGTGATCGC 1813
 TCACAACGCT CCCGATGTGC CGGTGCTGAA CTACTTGCGC GGCGACCCGG GCAACGGGGA 1873
 GGGCATGTTG GTGTCCGGTC TGGTGTGGC GGTGATGGTC GTTCCCATTA TCGCCACCAC 1933
 CACTCATGAC CTGTTCCGGC AGGTGCCGGT GTTGCCCCGG GAGGGCGCGA TCGGGAATTC 1993

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

Val Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
 1 5 10 15
 Leu Leu Leu Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
 20 25 30
 Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 35 40 45
 Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 50 55 60
 Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 65 70 75 80
 Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 85 90 95
 Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
 100 105 110
 Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
 115 120 125
 Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys

| | | | | |
|---|---|-----|-----|-----|
| 130 | | 135 | | 140 |
| Leu Asn Gly Lys Val | Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr | | | |
| 145 | 150 | 155 | | 160 |
| Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro | | | | |
| | 165 | 170 | | 175 |
| Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr | | | | |
| | 180 | 185 | | 190 |
| Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly | | | | |
| | 195 | 200 | | 205 |
| Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly | | | | |
| | 210 | 215 | | 220 |
| Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu | | | | |
| | 225 | 230 | 235 | 240 |
| Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala | | | | |
| | 245 | 250 | | 255 |
| Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn | | | | |
| | 260 | 265 | | 270 |
| Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala Gly Phe | | | | |
| | 275 | 280 | | 285 |
| Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro | | | | |
| | 290 | 295 | | 300 |
| Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn | | | | |
| | 305 | 310 | 315 | 320 |
| Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu | | | | |
| | 325 | 330 | | 335 |
| His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val | | | | |
| | 340 | 345 | | 350 |
| His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu | | | | |
| | 355 | 360 | | 365 |
| Ile Ala Thr Ile Ser Ser | | | | |
| 370 | | | | |

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

| | | | | | | |
|-------------|------------|-------------|------------|------------|------------|------|
| TGTTCTTCGA | CGGCAGGCTG | GTGGAGGAAG | GGCCCACCGA | ACAGCTGTTC | TCCTCGCCGA | 60 |
| AGCATGCGGA | AACCGCCCGA | TACGTCGCCG | GACTGTCGGG | GGACGTCAAG | GACGCCAAGC | 120 |
| GCGGAAATTG | AAGAGCACAG | AAAGGTATGG | CGTGAAAATT | CGTTTGCATA | CGCTGTTGGC | 180 |
| CGTGTTGACC | GCTGCGCCGC | TGCTGCTAGC | AGCGGCGGGC | TGTGGCTCGA | AACCACCGAG | 240 |
| CGGTTGCGCT | GAAACGGGCG | CCGGCGCCGG | TACTGTCGCG | ACTACCCCGG | CGTCGTCGCC | 300 |
| GGTGACGTTG | GCGGAGACCG | GTAGCACGCT | GCTCTACCCG | CTGTTCAACC | TGTGGGGTCC | 360 |
| GGCCTTTTAC | GAGAGGTATC | CGAACGTCAC | GATCACCGCT | CAGGGCACCG | GTTCTGGTGC | 420 |
| CGGGATCGCG | CAGGCCGCCG | CCGGGACGGT | CAACATTGGG | GCCTCCGACG | CCTATCTGTC | 480 |
| GGAAGGTGAT | ATGGCCGCGC | ACAAGGGGCT | GATGAACATC | GCGCTAGCCA | TCTCCGCTCA | 540 |
| GCAGGTCAAC | TACAACCTGC | CCGGAGTGAG | CGAGCACCTC | AAGCTGAACG | GAAAAGTCCT | 600 |
| GGCGGCCATG | TACCAGGGCA | CCATCAAAAC | CTGGGACGAC | CCGCAGATCG | CTGCGCTCAA | 660 |
| CCCCGGCGTG | AACCTGCCCC | GCACCGCGGT | AGTTCCGCTG | CACCGCTCCG | ACGGGTCCGG | 720 |
| TGACACCTTC | TTGTTTACCC | AGTACCTGTC | CAAGCAAGAT | CCCAGGGGCT | GGGGCAAGTC | 780 |
| GCCCGGCTTC | GGCACCACCG | TCGACTTCCC | GGCGGTGCCG | GGTGCGCTGG | GTGAGAACGG | 840 |
| CAACGGCGGC | ATGGTGACCG | GTTGCGCCGA | GACACCGGGC | TGCGTGGCCT | ATATCGGCAT | 900 |
| CAGCTTCCTC | GACCAGGCCA | GTCAACGGGG | ACTCGGCGAG | GCCCAACTAG | GCAATAGCTC | 960 |
| TGGCAATTTT | TTGTTGCCCG | ACGCGCAAAG | CATTCAGGCC | GCGGCGGCTG | GCTTCGCATC | 1020 |
| GAAAACCCCG | GCGAACCAGG | CGATTTTCGAT | GATCGACGGG | CCCGCCCCGG | ACGGCTACCC | 1080 |
| GATCATCAAC | TACGAGTACG | CCATCGTCAA | CAACCGGCAA | AAGGACGCCG | CCACCGCGCA | 1140 |
| GACCTTGCAG | GCATTTCTGC | ACTGGGCGAT | CACCGACGGC | AACAAGGCCT | CGTTCCTCGA | 1200 |
| CCAGGTTTCAT | TTCCAGCCGC | TGCCGCCCGC | GGTGGTGAAG | TTGTCTGACG | CGTTGATCGC | 1260 |
| GACGATTTCC | AGCTAGCCTC | GTTGACCACC | ACGCGACAGC | AACCTCCGTC | GGGCCATCGG | 1320 |
| GCTGCTTTGC | GGAGCATGCT | GGCCCGTGCC | GGTGAAGTCG | GCCGCGCTGG | CCCGGCCATC | 1380 |
| CGGTGGTTGG | GTGGGATAGG | TGCGGTGATC | CCGCTGCTTG | CGCTGGTCTT | GGTGCTGGTG | 1440 |
| GTGCTGGTCA | TCGAGGCGAT | GGGTGCGATC | AGGCTCAACG | GGTTGCATTT | CTTCACCGCC | 1500 |
| ACCGAATGGA | ATCCAGGCAA | CACCTACGGC | GAAACCGTTG | TCACCGACGC | GTCGCCCATC | 1560 |
| CGGTCGGCGC | CTACTACGGG | GCGTTGCCGC | TGATCGTCGG | GACGCTGGCG | ACCTCGGCAA | 1620 |

TCGCCCTGAT CATCGCGGTG CCGGTCTCTG TAGGAGCGGC GCTGGTGATC GTGGAACGGC 1680
 TGCCGAAACG GTTGGCCGAG GCTGTGGGAA TAGTCCTGGA ATTGCTCGCC GGAATCCCCA 1740
 GCGTGGTCGT CGGTTTGTGG GGGGCAATGA CGTTCGGGCC GTTCATCGCT CATCACATCG 1800
 CTCCGGTGAT CGCTCACAAC GCTCCCGATG TGCCGGTGCT GAACTACTTG CGCGGCGACC 1860
 CGGGCAACGG GGAGGGCATG TTGGTGTCCG GTCTGGTGTT GGCGGTGATG GTCGTTCCCA 1920
 TTATCGCCAC CACCACTCAT GACCTGTTCC GGCAGGTGCC GGTGTTGCCC CGGGAGGGCG 1980
 CGATCGGGAA TTC 1993

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | Ile | Arg | Leu | His | Thr | Leu | Leu | Ala | Val | Leu | Thr | Ala | Ala | Pro | 1 | 5 | 10 | 15 |
| Leu | Leu | Leu | Ala | Ala | Ala | Gly | Cys | Gly | Ser | Lys | Pro | Pro | Ser | Gly | Ser | 20 | 25 | 30 | |
| Pro | Glu | Thr | Gly | Ala | Gly | Ala | Gly | Thr | Val | Ala | Thr | Thr | Pro | Ala | Ser | 35 | 40 | 45 | |
| Ser | Pro | Val | Thr | Leu | Ala | Glu | Thr | Gly | Ser | Thr | Leu | Leu | Tyr | Pro | Leu | 50 | 55 | 60 | |
| Phe | Asn | Leu | Trp | Gly | Pro | Ala | Phe | His | Glu | Arg | Tyr | Pro | Asn | Val | Thr | 65 | 70 | 75 | 80 |
| Ile | Thr | Ala | Gln | Gly | Thr | Gly | Ser | Gly | Ala | Gly | Ile | Ala | Gln | Ala | Ala | 85 | 90 | 95 | |
| Ala | Gly | Thr | Val | Asn | Ile | Gly | Ala | Ser | Asp | Ala | Tyr | Leu | Ser | Glu | Gly | 100 | 105 | 110 | |
| Asp | Met | Ala | Ala | His | Lys | Gly | Leu | Met | Asn | Ile | Ala | Leu | Ala | Ile | Ser | 115 | 120 | 125 | |
| Ala | Gln | Gln | Val | Asn | Tyr | Asn | Leu | Pro | Gly | Val | Ser | Glu | His | Leu | Lys | 130 | 135 | 140 | |
| Leu | Asn | Gly | Lys | Val | Leu | Ala | Ala | Met | Tyr | Gln | Gly | Thr | Ile | Lys | Thr | 145 | 150 | 155 | 160 |

205220 E4243001

Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
 165 170 175
 Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
 180 185 190
 Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
 195 200 205
 Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 210 215 220
 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 225 230 235 240
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 245 250 255
 Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 260 265 270
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe
 275 280 285
 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300
 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335
 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365
 Ile Ala Thr Ile Ser Ser
 370

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGTCTTGACC ACCACCTGGG TGTCGAAGTC GGTGCCCGGA TTGAAGTCCA GGTACTCGTG 60
 GGTGGGGCGG GCGAAACAAT AGCGACAAGC ATGCGAGCAG CCGCGGTAGC CGTTGACGGT 120

GTAGCGAAAC GGCAACGCGG CCGCGTTGGG CACCTTGTTT AGCGCTGATT TGCACAACAC 180
 CTCGTGGAAG GTGATGCCGT CGAATTGTGG CGCGCGAACG CTGCGGACCA GGCCGATCCG 240
 CTGCAACCCG GCAGCGCCCG TCGTCAACGG GCATCCCGTT CACCGCGACG GCTTGCCGGG 300
 CCCAACGCAT ACCATTATTC GAACAACCGT TCTATACTTT GTCAACGCTG GCCGCTACCG 360
 AGCGCCGCAC AGGATGTGAT ATGCCATCTC TGCCCGCACA GACAGGAGCC AGGCCTTATG 420
 ACAGCATTCG GCGTCGAGCC CTACGGGCAG CCGAAGTACC TAGAAATCGC CGGGAAGCGC 480
 ATGGCGTATA TCGACGAAGG CAAGGGTGAC GCCATCGTCT TTCAGCACGG CAACCCACG 540
 TCGTCTTACT TGTGGCGCAA CATCATGCCG CACTTGGAAG GGCTGGGCCG GCTGGTGGCC 600
 TGCGATCTGA TCGGGATGGG CGCGTCGGAC AAGCTCAGCC CATCGGGACC CGACCGCTAT 660
 AGCTATGGCG AGCAACGAGA CTTTTTGTTT GCGCTCTGGG ATGCGCTCGA CCTCGGCGAC 720
 CACGTGGTAC TGGTGCTGCA CGACTGGGGC TCGGCGCTCG GCTTCGACTG GGCTAACCAG 780
 CATCGCGACC GAGTGCAGGG GATCGCGTTC ATGGAAGCGA TCGTCACCCC GATGACGTGG 840
 GCGGACTGGC CGCCGGCCGT GCGGGGTGTG TTCCAGGGTT TCCGATCGCC TCAAGGCGAG 900
 CCAATGGCGT TGGAGCACA CATCTTTGTC GAACGGGTGC TGCCCGGGGC GATCCTGCGA 960
 CAGCTCAGCG ACGAGGAAAT GAACCACTAT CGGCGGCCAT TCGTGAACGG CGGCGAGGAC 1020
 CGTCGCCCCA CGTTGTCTGT GCCACGAAAC CTTCCAATCG ACGGTGAGCC CGCCGAGGTC 1080
 GTCGCGTTGG TCAACGAGTA CCGGAGCTGG CTCGAGGAAA CCGACATGCC GAAACTGTTC 1140
 ATCAACGCCG AGCCCGGCGC GATCATCACC GGCCGCATCC GTGACTATGT CAGGAGCTGG 1200
 CCCAACCAGA CCGAAATCAC AGTGCCCGGC GTGCATTTTC TTCAGGAGGA CAGCGATGGC 1260
 GTCGTATCGT GGGCGGGCGC TCGGCAGCAT CGGCGACCTG GGAGCGCTCT CATTTACGA 1320
 GACCAAGAAT GTGATTTCCG GCGAAGGCGG CGCCCTGCTT GTCAACTCAT AAGACTTCCT 1380
 GCTCCGGGCA GAGATTCTCA GGGAAAAGGG CACCAATCGC AGCCGCTTCC TTCGCAACGA 1440
 GGTCGACAAA TATACGTGGC AGGACAAAGG TCTTCCTATT TGCCCAGCGA ATTAGTCGCT 1500
 GCCTTTCTAT GGGCTCAGTT CGAGGAAGCC GAGCGGATCA CGCGTATCCG ATTGGACCTA 1560
 TGGAACCGGT ATCATGAAAG CTTCGAATCA TTGGAACAGC GGGGGCTCCT GCGCCGTCCG 1620
 ATCATCCAC AGGGCTGCTC TCACAACGCC CACATGTACT ACGTGTTACT AGCGCCAGC 1680
 GCCGATCGGG AGGAGGTGCT GGCGCGTCTG ACGAGCGAAG GTATAGGCGC GGTCTTTCAT 1740

TACGTGCCGC TTCACGATTC GCCGGCCGGG CGTCGCT

1777

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

| | |
|---|-----|
| GAGATTGAAT CGTACCGGTC TCCTTAGCGG CTCCGTCCCG TGAATGCCCA TATCACGCAC | 60 |
| GGCCATGTTT TGGCTGTCGA CCTTCGCCCC ATGCCCGGAC GTTGGTAAAC CCAGGGTTTG | 120 |
| ATCAGTAATT CCGGGGGACG GTTGCGGGAA GCGCGCCAGG ATGTGCGTGA GCCGCGGCGC | 180 |
| CGCCGTGCGC CAGGCGACCG CTGGATGCTC AGCCCCGGTG CCGCGACGTA GCCAGCGTTT | 240 |
| GGCGCGTGTC GTCCACAGTG GTACTCCGGT GACGACGCGG CGCGGTGCCT GGGTGAAGAC | 300 |
| CGTGACCGAC GCCGCCGATT CAGA | 324 |

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

| | |
|---|-----|
| GCGGTACCGC CGCGTTGCGC TGGCACGGGA CCTGTACGAC CTGAACCACT TCGCCTCGCG | 60 |
| AACGATTGAC GAACCGCTCG TCGGGCGGCT GTGGGTGCTC AAGGTGTGGG GTGATGTCGT | 120 |
| CGATGACCGG CGCGGCACCC GGCCACTACG CGTCGAAGAC GTCCTCGCCG CCCGCAGCGA | 180 |
| GCACGACTTC CAGCCCCGACT CGATCGGCGT GCTGACCCGT CCTGTGCTA TGGCTGCCTG | 240 |
| GGAAGCTCGC GTTCGGAAGC GATTTGCGTT CCTCACTGAC CTCGACGCCG ACGAGCAGCG | 300 |
| GTGGGCCCGC TGCACGAAC GGCACCGCCG CGAAGTGGAG AACGCGCTGG CGGTGCTGCG | 360 |
| GTCCTGATCA ACCTGCCGGC GATCGTGCCG TTCCGCTGGC ACGGTTGCGG CTGGACGCGG | 420 |
| CTGAATCGAC TAGATGAGAG CAGTTGGGCA CGAATCCGGC TGTGGTGGTG AGCAAGACAC | 480 |
| GAGTACTGTC ATCACTATTG GATGCACTGG ATGACCGGCC TGATTCAGCA GGACCAATGG | 540 |
| AACTGCCCCG GGCAAAACGT CTCGGAGATG ATCGGCGTCC CCTCGGAACC CTGCGGTGCT | 600 |
| GGCGTCATTC GGACATCGGT CCGGCTCGCG GGATCGTGGT GACGCCAGCG CTGAAGGAGT | 660 |

10084843.02502

GGAGCGCGGC GGTGCACGCG CTGCTGGACG GCCGGCAGAC GGTGCTGCTG CGTAAGGGCG 720
 GGATCGGCGA GAAGCGCTTC GAGGTGGCGG CCCACGAGTT CTTGTTGTTC CCGACGGTCG 780
 CGCACAGCCA CGCCGAGCGG GTTCGCCCCG AGCACCGCGA CCTGCTGGGC CCGGCGGCCG 840
 CCGACAGCAC CGACGAGTGT GTGCTACTGC GGGCCGCAGC GAAAGTTGTT GCCGCACTGC 900
 CGGTTAACCG GCCAGAGGGT CTGGACGCCA TCGAGGATCT GCACATCTGG ACCGCCGAGT 960
 CGGTGCGCGC CGACCGGCTC GACTTTCGGC CCAAGCACAA ACTGGCCGTC TTGGTGGTCT 1020
 CGGCGATCCC GCTGGCCGAG CCGGTCCGGC TGGCGCGTAG GCCCGAGTAC GGC GGTTGCA 1080
 CCAGCTGGGT GCAGCTGCCG GTGACGCCGA CGTTGGCGGC GCCGGTGCAC GACGAGGCCG 1140
 CGCTGGCCGA GGTCGCCGCC CGGGTCCGCG AGGCCGTGGG TTGACTGGGC GGCATCGCTT 1200
 GGGTCTGAGC TGTACGCCCA GTCGGCGCTG CGAGTGATCT GCTGTCGGTT CGGTCCCTGC 1260
 TGGCGTCAAT TGACGGCGCG GGCAACAGCA GCATTGGCGG CGCCATCCTC CGCGCGGCCG 1320
 GCGCCACCG CTACAACC 1338

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

CCGGCGGCAC CGGCGGCACC GCGGTACCG GCGGCAACGG CGCTGACGCC GCTGCTGTGG 60
 TGGGCTTCGG CGGCAACGGC GACCCTGGCT TCGCTGGCGG CAAAGGCGGT AACGGCGGAA 120
 TAGGTGGGGC CGCGGTGACA GGCGGGGTCG CCGGCGACGG CGGCACCGGC GGCAAAGGTG 180
 GCACCGGCGG TGCCGGCGGC GCCGGCAACG ACGCCGGCAG CACCGGCAAT CCCGGCGGTA 240
 AGGGCGGCGA CGGCGGGATC GCGGGTGCCG GCGGGGCCGG CGGCGCGGCC GGCACCGGCA 300
 ACGGCGGCCA TGCCGGCAAC C 321

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```

GAAGACCCGG CCCC GCCATA TCGATCGGCT CGCCGACTAC TTTCGCCGAA CGTGCACGCG      60
GCGGCGTCGG GCTGATCATC ACCGGTGGCT ACGCGCCCAA CCGCACC GGA TGGCTGCTGC      120
CGTTGCCTC CGAACTCGTC ACTTCGGCGC AAGCCCGACG GCACCGCCGA ATCACCAGGG      180
CGGTCCACGA TTCGGGTGCA AAGATCCTGC TGCAAATCCT GCACGCCGGA CGCTACGCCT      240
ACCACCCACT TCGGGTCAGC GCCTCGCCGA TCAAGGCGCC GATCACCCCG TTTCGTCCGC      300
GAGCACTATC GGCTCGCGGG GTCGAAGCGA CCATCGCGGA TTTCGCCCGC TCGCGCAGT      360
TGGCCCGCGA TGCCGGCTAC GACGGCGTCG AAATCATGGG CAGCGAAGGG TATCTGCTCA      420
ATCAGTTCCT GGCGCCGCGC ACCAACAAGC GCACCGACTC GTGGGGCGGC ACACCGGCCA      480
ACCGTCGCCG GT                                         492

```

(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```

Phe Ala Gln His Leu Val Glu Gly Asp Ala Val Glu Leu Trp Arg Ala
1              5              10              15

Asn Ala Ala Asp Gln Ala Asp Pro Leu Gln Pro Gly Ser Ala Arg Arg
                20              25              30

Gln Arg Ala Ser Arg Ser Pro Arg Arg Leu Ala Gly Pro Asn Ala Tyr
35              40              45

His Tyr Ser Asn Asn Arg Ser Ile Leu Cys Gln Arg Trp Pro Leu Pro
50              55              60

Ser Ala Ala Gln Asp Val Ile Cys His Leu Cys Pro His Arg Gln Glu
65              70              75              80

Pro Gly Leu Met Thr Ala Phe Gly Val Glu Pro Tyr Gly Gln Pro Lys
85              90              95

Tyr Leu Glu Ile Ala Gly Lys Arg Met Ala Tyr Ile Asp Glu Gly Lys
100             105             110

Gly Asp Ala Ile Val Phe Gln His Gly Asn Pro Thr Ser Ser Tyr Leu
115             120             125

Trp Arg Asn Ile Met Pro His Leu Glu Gly Leu Gly Arg Leu Val Ala

```

| | | |
|---|-----|-------------|
| 130 | 135 | 140 |
| Cys Asp Leu Ile Gly Met Gly Ala Ser Asp Lys Leu Ser Pro Ser Gly | | |
| 145 | 150 | 155 160 |
| Pro Asp Arg Tyr Ser Tyr Gly Glu Gln Arg Asp Phe Leu Phe Ala Leu | | |
| | 165 | 170 175 |
| Trp Asp Ala Leu Asp Leu Gly Asp His Val Val Leu Val Leu His Asp | | |
| | 180 | 185 190 |
| Trp Gly Ser Ala Leu Gly Phe Asp Trp Ala Asn Gln His Arg Asp Arg | | |
| | 195 | 200 205 |
| Val Gln Gly Ile Ala Phe Met Glu Ala Ile Val Thr Pro Met Thr Trp | | |
| | 210 | 215 220 |
| Ala Asp Trp Pro Pro Ala Val Arg Gly Val Phe Gln Gly Phe Arg Ser | | |
| | 225 | 230 235 240 |
| Pro Gln Gly Glu Pro Met Ala Leu Glu His Asn Ile Phe Val Glu Arg | | |
| | 245 | 250 255 |
| Val Leu Pro Gly Ala Ile Leu Arg Gln Leu Ser Asp Glu Glu Met Asn | | |
| | 260 | 265 270 |
| His Tyr Arg Arg Pro Phe Val Asn Gly Gly Glu Asp Arg Arg Pro Thr | | |
| | 275 | 280 285 |
| Leu Ser Trp Pro Arg Asn Leu Pro Ile Asp Gly Glu Pro Ala Glu Val | | |
| | 290 | 295 300 |
| Val Ala Leu Val Asn Glu Tyr Arg Ser Trp Leu Glu Glu Thr Asp Met | | |
| | 305 | 310 315 320 |
| Pro Lys Leu Phe Ile Asn Ala Glu Pro Gly Ala Ile Ile Thr Gly Arg | | |
| | 325 | 330 335 |
| Ile Arg Asp Tyr Val Arg Ser Trp Pro Asn Gln Thr Glu Ile Thr Val | | |
| | 340 | 345 350 |
| Pro Gly Val His Phe Val Gln Glu Asp Ser Asp Gly Val Val Ser Trp | | |
| | 355 | 360 365 |
| Ala Gly Ala Arg Gln His Arg Arg Pro Gly Ser Ala Leu Ile Ser Arg | | |
| | 370 | 375 380 |
| Asp Gln Glu Cys Asp Phe Arg Arg Arg Arg Arg Pro Ala Cys Gln Leu | | |
| | 385 | 390 395 400 |
| Ile Arg Leu Pro Ala Pro Gly Arg Asp Ser Gln Gly Lys Gly His Gln | | |
| | 405 | 410 415 |
| Ser Gln Pro Leu Pro Ser Gln Arg Gly Arg Gln Ile Tyr Val Ala Gly | | |
| | 420 | 425 430 |

Gln Arg Ser Ser Tyr Leu Pro Ser Glu Leu Val Ala Ala Phe Leu Trp
 435 440 445

Ala Gln Phe Glu Glu Ala Glu Arg Ile Thr Arg Ile Arg Leu Asp Leu
 450 455 460

Trp Asn Arg Tyr His Glu Ser Phe Glu Ser Leu Glu Gln Arg Gly Leu
 465 470 475 480

Leu Arg Arg Pro Ile Ile Pro Gln Gly Cys Ser His Asn Ala His Met
 485 490 495

Tyr Tyr Val Leu Leu Ala Pro Ser Ala Asp Arg Glu Glu Val Leu Ala
 500 505 510

Arg Leu Thr Ser Glu Gly Ile Gly Ala Val Phe His Tyr Val Pro Leu
 515 520 525

His Asp Ser Pro Ala Gly Arg Arg
 530 535

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 284 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Asn Glu Ser Ala Pro Arg Ser Pro Met Leu Pro Ser Ala Arg Pro Arg
 1 5 10 15

Tyr Asp Ala Ile Ala Val Leu Leu Asn Glu Met His Ala Gly His Cys
 20 25 30

Asp Phe Gly Leu Val Gly Pro Ala Pro Asp Ile Val Thr Asp Ala Ala
 35 40 45

Gly Asp Asp Arg Ala Gly Leu Gly Val Asp Glu Gln Phe Arg His Val
 50 55 60

Gly Phe Leu Glu Pro Ala Pro Val Leu Val Asp Gln Arg Asp Asp Leu
 65 70 75 80

Gly Gly Leu Thr Val Asp Trp Lys Val Ser Trp Pro Arg Gln Arg Gly
 85 90 95

Ala Thr Val Leu Ala Ala Val His Glu Trp Pro Pro Ile Val Val His
 100 105 110

Phe Leu Val Ala Glu Leu Ser Gln Asp Arg Pro Gly Gln His Pro Phe
 115 120 125

Asp Lys Asp Val Val Leu Gln Arg His Trp Leu Ala Leu Arg Arg Ser
 130 135 140
 Glu Thr Leu Glu His Thr Pro His Gly Arg Arg Pro Val Arg Pro Arg
 145 150 155 160
 His Arg Gly Asp Asp Arg Phe His Glu Arg Asp Pro Leu His Ser Val
 165 170 175
 Ala Met Leu Val Ser Pro Val Glu Ala Glu Arg Arg Ala Pro Val Val
 180 185 190
 Gln His Gln Tyr His Val Val Ala Glu Val Glu Arg Ile Pro Glu Arg
 195 200 205
 Glu Gln Lys Val Ser Leu Leu Ala Ile Ala Ile Ala Val Gly Ser Arg
 210 215 220
 Trp Ala Glu Leu Val Arg Arg Ala His Pro Asp Gln Ile Ala Gly His
 225 230 235 240
 Gln Pro Ala Gln Pro Phe Gln Val Arg His Asp Val Ala Pro Gln Val
 245 250 255
 Arg Arg Arg Gly Val Ala Val Leu Lys Asp Asp Gly Val Thr Leu Ala
 260 265 270
 Phe Val Asp Ile Arg His Ala Leu Pro Gly Asp Phe
 275 280

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

ATGAACATGT CGTCGGTGGT GGGTCGCAAG GCCTTTGCGC GATTGCGCCG CTACTCCTCC 60
 GCCATGCACG CGATCGCCCG TTTCTCCGAT GCGTTGCGCC AAGAGCTGCG GGGTAGCGGA 120
 ATCGCCGTCT CGGTGATCCA CCCGGCGCTG ACCCAGACAC CGCTGTTGGC CAACGTCGAC 180
 CCCGCCGACA TGCCGCCGCC GTTTCGCAGC CTCACGCCCA TTCCC GTTCA CTGGGTCGCG 240
 GCAGCGGTGC TTGACGGTGT GGCG 264

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1171 base pairs

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(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

| | |
|---|------|
| TAGTCGGCGA CGATGACGTC GCGGTCCAGG CCGACCGCTT CAAGCACCAG CGCGACCACG | 60 |
| AAGCCGGTGC GATCCTTACC CGCGAAGCAG TGGGTGAGCA CCGGGCGTCC GCGGCAAGC | 120 |
| AGTGTGACGA CACGATGTAG CGCGCGCTGT GCTCCATTGC GCGTTGGGAA TTGGCGATAC | 180 |
| TCGTGCGTCA TGTAGCGGGT GGCCGCGTCA TTTATCGACT GGCTGGATTC GCCGGACTCG | 240 |
| CCGTTGGACC CGTCATTGGT TAGCAGCCTC TTGAATGCGG TTTCGTGCGG CGCTGAGTCG | 300 |
| TCGGCGTCAT CATCGGCGAG GTCGGGGAAC GGCAGCAGGT GGACGTCGAT GCCGTCCGGA | 360 |
| ACCCGTCCTG GACCGCGGCG GGCAACCTCC CGGGACGACC GCAGGTCGGC AACGTCGGTG | 420 |
| ATCCCCAGCC GGCGCAGCGT TGCCCCCTCGT GCCGAATTCG GCACGAGGCT GGCGAGCCAC | 480 |
| CGGGCATCAC CAAGCAACGC TTGCCCAGTA CGGATCGTCA CTTCCGCATC CGGCAGACCA | 540 |
| ATCTCCTCGC CGCCCATCGT CAGATCCCGC TCGTGCGTTG ACAAGAACGG CCGCAGATGT | 600 |
| GCCAGCGGGT ATCGGAGATT GAACCGCGCA CGCAGTTCTT CAATCGCTGC GCGCTGCCGC | 660 |
| ACTATTGGCA CTTTCCGGCG GTCGCGGTAT TCAGCAAGCA TGCAGTCTC GACGAACTCG | 720 |
| CCCCACGTAA CCCACGGCGT AGCTCCCGGC GTGACGCGGA GGATCGGCGG GTGATCTTTG | 780 |
| CCGCCACGCT CGTAGCCGTT GATCCACCGC TTCGCGGTGC CGGCGGGGAG GCCGATCAGC | 840 |
| TTATCGACCT CGGCGTATGC CGACGGCAAG CTGGGCGCGT TCGTCGAGGT CAAGAACTCC | 900 |
| ACCATCGGCA CCGGCACCAA GGTGCCGCAC CTGACCTACG TCGGCGACGC CGACATCGGC | 960 |
| GAGTACAGCA ACATCGGCGC CTCCAGCGTG TTCGTCAACT ACGACGGTAC GTCCAAACGG | 1020 |
| CGCACCACCG TCGGTTTCGCA CGTACGGACC GGGTCCGACA CCATGTTTCGT GGCCCCAGTA | 1080 |
| ACCATCGGCG ACGGCGCGTA TACCGGGGCC GGCACAGTGG TGCGGGAGGA TGTCCC GCCG | 1140 |
| GGGGCGCTGG CAGTGTCGGC GGGTCCGCAA C | 1171 |

(2) INFORMATION FOR SEQ ID NO:165:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

205220 E4B4B00T

GCAAAGGCGG CACCGGCGGG GCCGGCATGA ACAGCCTCGA CCCGCTGCTA GCCGCCCAAG 60
 ACGGCGGCCA AGGCGGCACC GGCGGCACCG GCGGCAACGC CGGCGCCGGC GGCACCAGCT 120
 TCACCCAAGG CGCCGACGGC AACGCCGGCA ACGGCGGTGA CGGCGGGGTC GGCGGCAACG 180
 GCGGAAACGG CGGAAACGGC GCAGACAACA CCACCACCGC CGCCGCC 227

(2) INFORMATION FOR SEQ ID NO:166:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

CCTCGCCACC ATGGGCGGGC AGGGCGGTAG CGGTGGCGCC GGCTCTACCC CAGGCGCCAA 60
 GGGCGCCCAC GGCTTCACTC CAACCAGCGG CGGCGACGGC GGCGACGGCG GCAACGGCGG 120
 CAACTCCCAA GTGGTCGGCG GCAACGGCGG CGACGGCGGC AATGGCGGCA ACGGCGGCAG 180
 CGCCGGCACG GGCGGCAACG GCGGCCGCGG CGGCGACGGC GCGTTTGGTG GCATGAGTGC 240
 CAACGCCACC AACCCTGGTG AAAACGGGCC AAACGGTAAC CCCGCGGCA ACGGTGGCGC 300
 CGGC 304

(2) INFORMATION FOR SEQ ID NO:167:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1439 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GTGGGACGCT GCCGAGGCTG TATAACAAGG ACAACATCGA CCAGCGCCGG CTCGGTGAGC 60
 TGATCGACCT ATTTAACAGT GCGCGCTTCA GCCGGCAGGG CGAGCACCGC GCCCGGGATC 120
 TGATGGGTGA GGTCTACGAA TACTTCCTCG GCAATTTTCG TCGCGCGGAA GGAAGCGGG 180
 GTGGCGAGTT CTTTACCCCG CCCAGCGTGG TCAAGGTGAT CGTGGAGGTG CTGGAGCCGT 240
 CGAGTGGGCG GGTGTATGAC CCGTGCTGCG GTTCCGGAGG CATGTTTGTG CAGACCGAGA 300
 AGTTCATCTA CGAACACGAC GGCGATCCGA AGGATGTCTC GATCTATGGC CAGGAAAGCA 360
 TTGAGGAGAC CTGGCGGATG GCGAAGATGA ACCTCGCCAT CCACGGCATC GACAACAAGG 420

GGCTCGGCGC CCGATGGAGT GATACCTTCG CCCGCGACCA GCACCCGGAC GTGCAGATGG 480
 ACTACGTGAT GGCCAATCCG CCGTTCAACA TCAAAGACTG GGCCCGCAAC GAGGAAGACC 540
 CACGCTGGCG CTTCCGTGTT CCGCCCGCCA ATAACGCCAA CTACGCATGG ATTCAGCACA 600
 TCCTGTACAA CTTGGCGCCG GGAGGTCGGG CGGGCGTGGT GATGGCCAAC GGGTCGATGT 660
 CGTCGAACTC CAACGGCAAG GGGGATATTC GCGCGCAAAT CGTGGAGGCG GATTTGGTTT 720
 CCTGCATGGT CGCGTTACCC ACCCAGCTGT TCCGAGCAC CGGAATCCCG GTGTGCCTGT 780
 GGTTTTTCGC CAAAACAAG GCGGCAGGTA AGCAAGGGTC TATCAACCGG TCGGGGCAGG 840
 TGCTGTCAT CGACGCTCGT GAACTGGGCG ACCTAGTGGA CCGGGCCGAG CGGGCGCTGA 900
 CCAACGAGGA GATCGTCCGC ATCGGGGATA CCTTCCACGC GAGCACGACC ACCGGCAACG 960
 CCGGCTCCGG TGGTGCCGGC GGTAATGGGG GCACTGGCCT CAACGGCGCG GCGGGTGCTG 1020
 GCGGGGCCGG CGGCAACGCG GGTGTCGCCG GCGTGTCTT CGGCAACGCT GTGGGCGGCG 1080
 ACGGCGGCAA CGGCGGCAAC GCGGGCCACG GCGGCGACGG CACGACGGGC GCGCCGGCG 1140
 GCAAGGGCGG CAACGGCAGC AGCGGTGCCG CCAGCGGCTC AGGCGTCGTC AACGTCACCG 1200
 CCGGCCACGG CGGCAACGGC GGCAATGGCG GCAACGGCGG CAACGGCTCC GCGGGCGCCG 1260
 GCGGCCAGGG CGGTGCCGGC GGCAGCGCCG GCAACGGCGG CCACGGCGGC GGTGCCACCG 1320
 GCGGCGCCAG CGGCAAGGGC GGCAACGGCA CCAGCGGTGC CGCCAGCGGC TCAGGCGTCA 1380
 TCAACGTCAC CGCCGGCCAC GCGGGCAACG GCGGCAATGG CCGCAACGGC GGCAACGGC 1439

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GGGCCGGCGG GGCCGATTT TCTCGTGCCT TGATTGTCGC TGGGGATAAC GCGGGTGATG 60
 GTGGTAACGG CGGGATGGGC GGGGCTGGCG GGGCTGGCGG CCGGGCGGG GCCGGCGGCC 120
 TGATCAGCCT GCTGGGCGGC CAAGGCGCCG GCGGGGCCGG CGGGACCGGC GGGGCCGGCG 180
 GTGTTGGCGG TGACGGCGGG GCCGGCGGCC CCGGCAACCA GGCCTTCAAC GCAGGTGCCG 240
 GCGGGGCCGG CGGCCTGATC AGCCTGCTGG GCGGCCAAGG CGCCGGCGGG GCCGGCGGGA 300
 CCGGCGGGGC CGGCGGTGTT GGCGGTGAC 329

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GCAACGGTGG CAACGGCGGC ACCAGCACGA CCGTGGGGAT GGCCGGAGGT AACTGTGGTG 60
 CCGCCGGGCT GATCGGCAAC 80

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 392 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GGGCTGTGTC GCACTCACAC CGCCGCATTC GGCGACGTTG GCCGCCCAAT ATCCAGCTCA 60
 AGGCCTACTA CTTACCGTCG GAGGACCGCC GCATCAAGGT GCGGGTCAGC GCCCAAGGAA 120
 TCAAGGTCAT CGACCGCGAC GGGCATCGAG GCCGTCGTCG CGCGGCTCGG GCAGGATCCG 180
 CCCC GGCGCA CTTGCGCGC CAAGCGGGCT CATCGCTCCG AACGGCGGCG ATCCTGTGAG 240
 CACA ACTGAT GGCGCGCAAC GAGATTCGTC CAATTGTCAA GCCGTGTTCG ACCGCAGGGA 300
 CCGGTTATAC GTATGTCAAC CTATGTCACT CGCAAGAACC GGCATAACGA TCCCGTGATC 360
 CGCCGACAGC CCACGAGTGC AAGACCGTTA CA 392

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 535 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

ACCGGCGCCA CCGGCGGCAC CGGGTTCGCC GGTGGCGCCG GCGGGGCCGG CGGGCAGGGC 60
 GGTATCAGCG GTGCCGGCGG CACCAACGGC TCTGGTGGCG CTGGCGGCAC CGGCGGACAA 120
 GGCGGCGCCG GGGGCGCTGG CGGGGCCGGC GCCGATAACC CCACCGGCAT CGGCGGCGCC 180

GGCGGCACCG GCGGCACCGG CGGAGCGGCC GGAGCCGGCG GGGCCGGTGG CGCCATCGGT 240
 ACCGGCGGCA CCGGCGGCGC GGTGGGCAGC GTCGGTAACG CCGGGATCGG CGGTACCGGC 300
 GGTACGGGTG GTGTCGGTGG TGCTGGTGGT GCAGGTGCGG CTGCGGCCGC TGGCAGCAGC 360
 GCTACCGGTG GCGCCGGGTT CGCCGGCGGC GCCGGCGGAG AAGGCGGACC GGGCGGCAAC 420
 AGCGGTGTGG GCGGCACCAA CGGCTCCGGC GGCGCCGGCG GTGCAGGCGG CAAGGGCGGC 480
 ACCGGAGGTG CCGGCGGGTC CGGCGCGGAC AACCCACCG GTGCTGGTTT CGCCG 535

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CCGACGTCGC CGGGGCGATA CGGGGGTCAC CGACTACTAC ATCATCCGCA CCGAGAATCG 60
 GCCGCTGCTG CAACCGCTGC GGGCGGTGCC GGTATCGGA GATCCGCTGG CCGACCTGAT 120
 CCAGCCGAAC CTGAAGGTGA TCGTCAACCT GGGCTACGGC GACCCGAACT ACGGCTACTC 180
 GACGAGCTAC GCCGATGTGC GAACGCCGTT CGGGCTGTGG CCGAACGTGC CGCCTCAGGT 240
 CATCGCCGAT GCCCTGGCCG CCGGAACACA AGAAGGCATC CTTGACTTCA CGGCCGACCT 300
 GCAGGCGCTG TCCGCGCAAC CGCTCACGCT CCCGCAGATC CAGCTGCCGC AACCCGCCGA 360
 TCTGGTGGCC GCGGTGGCCG CCGCACCGAC GCCGGCCGAG GTGGTGAACA CGCTCGCCAG 420
 GATCATCTCA ACCAACTACG CCGTCCTGCT GCCACCGTG GACATCGCCC TCGCCTGGTC 480
 ACCACCCTGC CGCTGTACAC CACCCAACTG TTCGTCAGGC AACTCGCTGC GGGCAATCTG 540
 ATCAACGCGA TCGGCTATCC CCTGGCGGCC ACCGTAGGTT TAGGCACGAT CGATAGCGGG 600
 CGGCGTGGAA TTGCTACCC TCCTCGCGGC GGCCTCGGAC ACCGTTCGAA ACATCGAGGG 660
 CCTCGTCACC TAACGGATTG CCGACGGCAT 690

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

205220 24800T

ACGGTGACGG CGGTACTGGC GGC GGCCACG GCGGCAACGG CGGGAATCCC GGGTGGCTCT 60
 TGGGCACAGC CGGGGGTGGC GGCAACGGTG GCGCCGGCAG CACCGGTACT GCAGGTGGCG 120
 GCTCTGGGGG CACCGGCGGC GACGGCGGGA CCGGCGGGCG TGGCGGCCTG TTAATGGGCG 180
 CCGGCGCCGG CGGGCACGGT GGC ACTGGCG GCGCGGGCGG TGCCGGTGTC GACGGTGGCG 240
 GCGCCGGCGG GGCCGGCGGG GCCGGCGGCA ACGGCGGCGC CGGGGGTCAA GCCGCCCTGC 300
 TGTTCGGGCG CGGCGGCACC GCGGAGCCG GCGGCTACGG CGGCGATGGC GGTGGCGGCG 360
 GTGACGGCTT CGACGGCAG ATGGCCGGCC TGGGTGGTAC CGGTGGC 407

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GATCGGTCAG CGCATCGCCC TCGGCGGCAA GCGATTCCGC GGTCTCACCG AAGAACATCG 60
 TGCACGCGGC GGCGCGGACC AGCCCGCTGC GCTGCGGCGC GTCGAACGCC TCCAGCAGGC 120
 ACAGCCAGTC CTTGGCGGCC TGCGAGGCGA ACACGTCGGT GTCACCGGTG TAGATCGCCG 180
 GGATGCCCCG CTCCGCCAAC GCATTCCGGC ACGCCGCGC GTCTTTGTGA TGCTCGACGA 240
 TCACCGCGAT GTCTGCGGCC ACCACGGGCC GCCCGGCGAA GGTGGCCCCG CTGGCCAGTA 300
 GCGCCGCGAC GTCGGCGGCC AGGTCGTCGG GGATGTGCCG GCGCAGCGCT CCGGCGCGAC 360
 GCCCGAAAAA CGACCCCTCA CCCAGCTGGG TCCGCTGGC ATATCCCTTG CCGTCCTGGG 420
 CGATATTGGA CGCGCATGCC CCGACCGCGT ACAGGCCGGC CACCACCG 468

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GGTGGTAACG GCGGCCAGGG TGGCATCGGC GCGCCGGCG AGAGAGGCGC CGACGGCGCC 60
 GGCCCCAATG CTAACGGCGC AAACGGCGAG AACGGCGGTA GCGGTGGTAA CGGTGGCGAC 120

GGCGGCGCCG GCGGCAATGG CGGCGCGGGC GGCAACGCGC AGGCGGCCGG GTACACCGAC 180
GGCGCCACGG GCACCGGCGG CGACGGCGGC AACGGCGGC 219

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

TAGTCCGGC GAGGGCGGCA AGGGCGGCGA CGGTGGCCAC GCGGTGACG GCGTCGGCGG 60
CAACAGTTCC GTCACCCAAG GCGGCAGCGG CGGTGGCGGC GGCGCCGGCG GCGCCGGCGG 120
CAGCGGCTTT TTCGGCGGCA AGGGCGGCTT CGGCGGCGAC GCGGTTCAGG GCGGCCCCAA 180
CGGCGGCGGT ACCGTCGGCA CCGTGGCCGG TGGCGGCGGC AACGGCGGTG TCGGCGGCCG 240
GGGCGGCGAC GCGTCTTTG CCGGTGCCGG CGGCCAGGGC GGCCTCGGTG GGCAGGGCGG 300
CAATGGCGGC GGCTCCACCG GCGGCAACGG CGGCCTTGGC GGC CGGGCG GTGGCGGAGG 360
CAACGCCCCG GCTCGTGCCG AATCCGGGCT GACCATGGAC AGCGCGGCCA AGTTCGCTGC 420
CATCGCATCA GGC CGTACT GCCCGAACA CCTGGAACAT CACCCGAGTT AGCGGGGCGC 480
ATTTCCTGAT CACC 494

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GGGCCGGTGG TGCCGCGGGC CAGCTCTTCA GCGCCGAGG CGCGGCGGGT GCCGTTGGGG 60
TTGGCGGCAC CGGCGGCCAG GGTGGGGCTG GCGGTGCCGG AGCGGCCGGC GCCGACGCC 120
CCGCCAGCAC AGGTCTAACC GGTGGTACCG GGTTCGCTGG CGGGGCCGGC GGCCTCGGCG 180
GCCAGAGCGG CAACGCCATT GCCGGCGGCA TCAACGGCTC 220

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

| | |
|---|-----|
| ATGGCGGCAA CGGGGGCCCC GGCGGTGCTG GCGGGGCCGG CGACTACAAT TTCCAACGGC | 60 |
| GGGCAGGGTG GTGCCGGCGG CCAAGGCGGC CAAGGCGGCC TGGGCGGGGC AAGCACCACC | 120 |
| TGATCGGCCT AGCCGCACCC GGGAAAGCCG ATCCAACAGG CGACGATGCC GCCTTCCTTG | 180 |
| CCGCGTTGGA CCAGGCCGGC ATCACCTACG CTGACCCAGG CCACGCCATA ACGGCCGCCA | 240 |
| AGGCGATGTG TGGGCTGTGT GCTAACGGCG TAACAGGTCT ACAGCTGGTC GCGGACCTGC | 300 |
| GGGACTACAA TCCCGGGCTG ACCATGGACA GCGCGGCCAA GTTCGCTGCC ATCGCATCAG | 360 |
| GCGCGTACTG CCCCGAACAC CTGGAACA | 388 |

(2) INFORMATION FOR SEQ ID NO:179:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

| | |
|---|-----|
| GCAAAGGCGG CACCGGCGGG GCCGGCATGA ACAGCCTCGA CCCGCTGCTA GCCGCCAAG | 60 |
| ACGGCGGCCA AGGCGGCACC GGCGGCACCG GCGGCAACGC CGGCGCCGGC GGCACCAGCT | 120 |
| TCACCCAAGG CGCCGACGGC AACGCCGGCA ACGGCGGTGA CGGCGGGGTC GGCGGCAACG | 180 |
| GCGGAAACGG CGGAAACGGC GCAGACAACA CCACCACCGC CGCCGCCGGC ACCACAGGCG | 240 |
| GCGACGGCGG GGCCGGCGGG GCCGGCGGAA CCGGCGGAAC CGGCGGAGCC GCCGGCACCG | 300 |
| GCACCGGCGG CCAACAAGGC AACGGCGGCA ACGGCGGCAC CGGCGGCAAA GCGGCGACCG | 360 |
| GCGGCGACGG TGCACTCTCA GGCAGCACCG GTGGTGCCGG | 400 |

(2) INFORMATION FOR SEQ ID NO:180:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 538 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

| | |
|---|----|
| GGCAACGGCG GCAACGGCGG CATCGCCGGC ATTGGGCGGC AACGGCGTTC CGGGACGGGC | 60 |
|---|----|

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AGCGGCAACG GCGGCCAACG GCGGCAGCGG CGGCAACGGC GGCAACGCCG GCATGGGCGG 120
 CAACAGCGGC ACCGGCAGCG GCGACGGCGG TGCCGGCGGG AACGGCGGCG CGGCGGGCAC 180
 GGGCGGCACC GGGGGCGACG GCGGCCTCAC CGGTACTGGC GGCACCGGCG GCAGCGGTGG 240
 CACCGGCGGT GACGGCGGTA ACGGCGGCAA CGGAGCAGAT AACACCGCAA ACATGACTGC 300
 GCAGGCGGGC GGTGACGGTG GCAACGGCGG CGACGGTGGC TTCGGCGGCG GGGCCGGGGC 360
 CGGCGGCGGT GGCTTGACCG CTGGCGCCAA CGGCACCGGC GGGCAAGGCG GCGCCGGCGG 420
 CGATGGCGGC AACGGGGCCA TCGGCGGCCA CGGCCACTC ACTGACGACC CCGGCGGCAA 480
 CGGGGGCACC GGCGGCAACG GCGGCACCGG CGGCACCGGC GGC GCGGGCA TCGGCAGC 538

(2) INFORMATION FOR SEQ ID NO:181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GGGCCGGTGG TGCCCGGGG CAGCTCTTCA GCGCCGAGG CGCGGCGGGT GCCGTTGGGG 60
 TTGGCGGCAC CGGCGGCCAG GGTGGGGCTG GCGGTGCCGG AGCGGCCGGC GCCGACGCCC 120
 CCGCCAGCAC AGGTCTAACC GGTGGTACCG GGTTCGCTGG CGGGGCCGGC GGCCTCGGCG 180
 GCCACGGCGG CAACGCCATT GCCGGCGGCA TCAACGGCTC CGGTGGTGCC GCGGGCACC 239

(2) INFORMATION FOR SEQ ID NO:182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 985 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

AGCAGCGCTA CCGGTGGCGC CGGGTTCGCC GCGGCGGCCG GCGGAGAAGG CGGAGCGGGC 60
 GGCAACAGCG GTGTGGGCGG CACCAACGGC TCCGGCGGCG CCGGCGGTGC AGGCGGCAAG 120
 GCGGGCACC GAGGTGCCGG CGGGTCCGGC GCGGACAACC CCACCGGTGC TGGTTTCGCC 180
 GGTGGCGCCG GCGGCACAGG TGGCGCGGCC GCGCGCGGCG GGGCCGGCGG GCGGACCGGT 240
 ACCGGCGGCA CCGGCGGCGT TGTCGGCGCC ACCGGTAGTG CAGGCATCGG CGGGGCCGGC 300
 GGCCGCGGCG GTGACGGCGG CGATGGGGCC AGCGGTCTCG GCCTGGGCCT CTCCGGCTTT 360

GACGGCGGCC AAGGCGGCCA AGGCGGGGCC GGCGGCAGCG CCGGCGCCGG CGGCATCAAC 420
 GGGGCCGGCG GGGCCGGCGG CAACGGCGGC GACGGCGGGG ACGGCGCAAC CGGTGCCGCA 480
 GGTCTCGGCG ACAACGGCGG GGTGGCGGT GACGGTGGGG CCGGTGGCGC CGCCGGCAAC 540
 GGCGGCAACG CGGGCGTCGG CCTGACAGCC AAGGCCGGCG ACGGCGGCGC CGCGGGCAAT 600
 GGCGGCAACG GGGGCGCCGG CGGTGCTGGC GGGGCCGGCG ACAACAATTT CAACGGCGGC 660
 CAGGGTGGTG CCGGCGGCCA AGGCGGCCAA GGCGGCTTGG GCGGGGCAAG CACCACCTGA 720
 TCGGCCTAGC CGCACCCGGG AAAGCCGATC CAACAGGCGA CGATGCCGCC TTCCTTGCCG 780
 CGTTGGACCA GGCCGGCATC ACCTACGCTG ACCCAGGCCA CGCCATAACG GCCGCCAAGG 840
 CGATGTGTGG GCTGTGTGCT AACGGCGTAA CAGGTCTACA GCTGGTCGCG GACCTGCGGG 900
 AATACAATCC CGGGCTGACC ATGGACAGCG CGGCCAAGTT CGCTGCCATC GCATCAGGCG 960
 CGTACTGCCC CGAACACCTG GAACA 985

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCCG ATTCGCCGGG TTTCCCCACC 60
 CGAGGAAAGC CGCTACCAGA TGGCGCTGCC GAAGTAGGGC GATCCGTTCG CGATGCCGGC 120
 ATGAACGGGC GGCATCAAAT TAGTGACAGG ACCTTTCAGT TTAGCGACGA TAATGGCTAT 180
 AGCACTAAGG AGGATGATCC GATATGACGC AGTCGCAGAC CGTGACGGTG GATCAGCAAG 240
 AGATTTTGAA CAGGGCCAAC GAGGTGGAGG CCCCAGTGGC GGACCCACCG ACTGATGTCC 300
 CCATCACACC GTGCGAACTC ACGGCGGCTA AAAACGCCGC CCAACAGCTG GTATTGTCCG 360
 CCGACAACAT GCGGGAATAC CTGGCGGCCG GTGCCAAAGA GCGGCAGCGT CTGGCGACCT 420
 CGCTGCGCAA CGCGGCCAAG GCGTATGGCG AGGTTGATGA GGAGGCTGCG ACCGCGCTGG 480
 ACAACGACGG CGAAGGAACT GTGCAGGCAG AATCGGCCGG GGCCGTCGGA GGGGACAGTT 540
 CGGCCGAACT AACCAGATAC CCGAGGGTGG CCACGGCCGG TGAACCCAAC TTCATGGATC 600
 TCAAAGAAGC GGCAAGGAAG CTCGAAACGG GCGACCAAGG CGCATCGCTC GCGCACTTTG 660

CGGATGGGTG GAACACTTTC AACCTGACGC TGCAAGGCGA CGTCAAGCGG TTCCGGGGGT 720

TTGACAACCTG GGAAGGCGAT GCGGCTACCG CTTGCGAGGC TTCGCTCGAT CAACAACGGC 780

AATGGATACT CCACATGGCC AAATTGAGCG CTGCGATGGC CAAGCAGGCT CAATATGTCTG 840

CGCAGCTGCA CGTGTGGGCT AGGCGGGAAC ATCCGACTTA TGAAGACATA GTCGGGCTCG 900

AACGGCTTTA CGCGGAAAAC CCTTCGGCCC GCGACCAAAT TCTCCCGGTG TACGCGGAGT 960

ATCAGCAGAG GTCGGAGAAG GTGCTGACCG AATACAACAA CAAGGCAGCC CTGGAACCGG 1020

TAAACCCGCC GAAGCCTCCC CCCGCCATCA AGATCGACCC GCCCCCGCCT CCGCAAGAGC 1080

AGGGATTGAT CCCTGGCTTC CTGATGCCGC CGTCTGACGG CTCCGGTGTG ACTCCCGGTA 1140

CCGGGATGCC AGCCGCACCG ATGGTTCCGC CTACCGGATC GCCGGGTGGT GGCTCCCGG 1200

CTGACACGGC GCGCAGCTG ACGTCGGCTG GCGGGAAGC CGCAGCGCTG TCGGGCGACG 1260

TGGCGGTCAA AGCGGCATCG CTCGGTGGCG GTGGAGGCGG CGGGGTGCCG TCGGCGCCGT 1320

TGGGATCCGC GATCGGGGGC GCCGAATCGG TGCGGCCCGC TGGCGCTGGT GACATTGCCG 1380

GCTTAGGCCA GGAAGGGCC GCGGCGGCG CCGCGCTGGG CGGCGGTGGC ATGGGAATGC 1440

CGATGGGTGC CGCGCATCAG GGACAAGGGG GCGCCAAGTC CAAGGGTTCT CAGCAGGAAG 1500

ACGAGGCGCT CTACACCGAG GATCGGGCAT GGACCGAGGC CGTCATTGGT AACCCTCGGC 1560

GCCAGGACAG TAAGGAGTCG AAGTGAGCAT GGACGAATTG GACCCGCATG TCGCCCGGGC 1620

GTTGACGCTG GCGGCGCGGT TTCAGTCGGC CCTAGACGGG ACGCTCAATC AGATGAACAA 1680

CGGATCCTTC CGCGCCACCG ACGAAGCCGA GACCGTCGAA GTGACGATCA ATGGGCACCA 1740

GTGGCTCACC GGCCTGCGCA TCGAAGATGG TTTGCTGAAG AAGCTGGGTG CCGAGGCGGT 1800

GGCTCAGCGG GTCAACGAGG CGCTGCACAA TGCGCAGGCC GCGGCGTCCG CGTATAACGA 1860

CGCGGCGGGC GAGCAGCTGA CCGCTGCGTT ATCGGCCATG TCCCGCGCGA TGAACGAAGG 1920

AATGGCCTAA GCCCATTGTT GCGGTGGTAG CGACTACGCA CCGAATGAGC GCCGCAATGC 1980

GGTCATTAG CGCGCCCGAC ACGGCGTGAG TACGATTGT CAATGTTTTG ACATGGATCG 2040

GCCGGGTTCG GAGGGCGCCA TAGTCCTGGT CGCCAATATT GCCGAGCTA GCTGGTCTTA 2100

GGTTCGGTTA CGCTGGTTAA TTATGACGTC CGTTACCA 2138

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 460 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn
 1 5 10 15
 Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val
 20 25 30
 Pro Ile Thr Pro Cys Glu Leu Thr Ala Ala Lys Asn Ala Ala Gln Gln
 35 40 45
 Leu Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
 50 55 60
 Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Ala
 65 70 75 80
 Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
 85 90 95
 Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
 100 105 110
 Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
 115 120 125
 Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
 130 135 140
 Gln Gly Ala Ser Leu Ala His Phe Ala Asp Gly Trp Asn Thr Phe Asn
 145 150 155 160
 Leu Thr Leu Gln Gly Asp Val Lys Arg Phe Arg Gly Phe Asp Asn Trp
 165 170 175
 Glu Gly Asp Ala Ala Thr Ala Cys Glu Ala Ser Leu Asp Gln Gln Arg
 180 185 190
 Gln Trp Ile Leu His Met Ala Lys Leu Ser Ala Ala Met Ala Lys Gln
 195 200 205
 Ala Gln Tyr Val Ala Gln Leu His Val Trp Ala Arg Arg Glu His Pro
 210 215 220
 Thr Tyr Glu Asp Ile Val Gly Leu Glu Arg Leu Tyr Ala Glu Asn Pro
 225 230 235 240
 Ser Ala Arg Asp Gln Ile Leu Pro Val Tyr Ala Glu Tyr Gln Gln Arg
 245 250 255
 Ser Glu Lys Val Leu Thr Glu Tyr Asn Asn Lys Ala Ala Leu Glu Pro
 260 265 270

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Val Asn Pro Pro Lys Pro Pro Pro Ala Ile Lys Ile Asp Pro Pro Pro
 275 280 285
 Pro Pro Gln Glu Gln Gly Leu Ile Pro Gly Phe Leu Met Pro Pro Ser
 290 295 300
 Asp Gly Ser Gly Val Thr Pro Gly Thr Gly Met Pro Ala Ala Pro Met
 305 310 315 320
 Val Pro Pro Thr Gly Ser Pro Gly Gly Gly Leu Pro Ala Asp Thr Ala
 325 330 335
 Ala Gln Leu Thr Ser Ala Gly Arg Glu Ala Ala Ala Leu Ser Gly Asp
 340 345 350
 Val Ala Val Lys Ala Ala Ser Leu Gly Gly Gly Gly Gly Gly Val
 355 360 365
 Pro Ser Ala Pro Leu Gly Ser Ala Ile Gly Gly Ala Glu Ser Val Arg
 370 375 380
 Pro Ala Gly Ala Gly Asp Ile Ala Gly Leu Gly Gln Gly Arg Ala Gly
 385 390 395 400
 Gly Gly Ala Ala Leu Gly Gly Gly Gly Met Gly Met Pro Met Gly Ala
 405 410 415
 Ala His Gln Gly Gln Gly Gly Ala Lys Ser Lys Gly Ser Gln Gln Glu
 420 425 430
 Asp Glu Ala Leu Tyr Thr Glu Asp Arg Ala Trp Thr Glu Ala Val Ile
 435 440 445
 Gly Asn Arg Arg Arg Gln Asp Ser Lys Glu Ser Lys
 450 455 460

(2) INFORMATION FOR SEQ ID NO:185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Ala Gly Asn Val Thr Ser Ala Ser Gly Pro His Arg Phe Gly Ala Pro
 1 5 10 15
 Asp Arg Gly Ser Gln Arg Arg Arg Arg His Pro Ala Ala Ser Thr Ala
 20 25 30
 Thr Glu Arg Cys Arg Phe Asp Arg His Val Ala Arg Gln Arg Cys Gly
 35 40 45

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Phe Pro Pro Ser Arg Arg Gln Leu Arg Arg Arg Val Ser Arg Glu Ala
 50 55 60
 Thr Thr Arg Arg Ser Gly Arg Arg Asn His Arg Cys Gly Trp His Pro
 65 70 75 80
 Gly Thr Gly Ser His Thr Gly Ala Val Arg Arg Arg His Gln Glu Ala
 85 90 95
 Arg Asp Gln Ser Leu Leu Leu Arg Arg Arg Gly Arg Val Asp Leu Asp
 100 105 110
 Gly Gly Gly Arg Leu Arg Arg Val Tyr Arg Phe Gln Gly Cys Leu Val
 115 120 125
 Val Val Phe Gly Gln His Leu Leu Arg Pro Leu Leu Ile Leu Arg Val
 130 135 140
 His Arg Glu Asn Leu Val Ala Gly Arg Arg Val Phe Arg Val Lys Pro
 145 150 155 160
 Phe Glu Pro Asp Tyr Val Phe Ile Ser Arg Met Phe Pro Pro Ser Pro
 165 170 175
 His Val Gln Leu Arg Asp Ile Leu Ser Leu Leu Gly His Arg Ser Ala
 180 185 190
 Gln Phe Gly His Val Glu Tyr Pro Leu Pro Leu Leu Ile Glu Arg Ser
 195 200 205
 Leu Ala Ser Gly Ser Arg Ile Ala Phe Pro Val Val Lys Pro Pro Glu
 210 215 220
 Pro Leu Asp Val Ala Leu Gln Arg Gln Val Glu Ser Val Pro Pro Ile
 225 230 235 240
 Arg Lys Val Arg Glu Arg Cys Ala Leu Val Ala Arg Phe Glu Leu Pro
 245 250 255
 Cys Arg Phe Phe Glu Ile His Glu Val Gly Phe Thr Gly Arg Gly His
 260 265 270
 Pro Arg Arg Ile Gly
 275

(2) INFORMATION FOR SEQ ID NO:186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

Arg Val Ala Ala Ser Phe Ile Asp Trp Leu Asp Ser Pro Asp Ser Pro
 1 5 10 15
 Leu Asp Pro Ser Leu Val Ser Ser Leu Leu Asn Ala Val Ser Cys Gly
 20 25 30
 Ala Glu Ser Ser Ala Ser Ser Ser Ala Arg Ser Gly Asn Gly Ser Arg
 35 40 45
 Trp Thr Ser Met Pro Ser Gly Thr Arg Pro Gly Pro Arg Arg Ala Thr
 50 55 60
 Ser Arg Asp Asp Arg Arg Ser Ala Thr Ser Val Ile Pro Ser Arg Arg
 65 70 75 80
 Ser Val Ala Pro Arg Ala Glu Phe Gly Thr Arg Leu Ala Ser His Arg
 85 90 95
 Ala Ser Pro Ser Asn Ala Cys Pro Val Arg Ile Val Thr Ser Ala Ser
 100 105 110
 Gly Arg Pro Ile Ser Ser Pro Pro Ile Val Arg Ser Arg Ser Cys Val
 115 120 125
 Asp Lys Asn Gly Arg Arg Cys Ala Ser Gly Tyr Arg Arg Leu Asn Arg
 130 135 140
 Ala Arg Ser Ser Ser Ile Ala Ala Arg Cys Arg Thr Ile Gly Thr Phe
 145 150 155 160
 Arg Arg Ser Arg Tyr Ser Ala Ser Met Arg Val Ser Thr Asn Ser Pro
 165 170 175
 His Val Thr His Gly Val Ala Pro Gly Val Thr Arg Arg Ile Gly Gly
 180 185 190

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Gln Glu Arg Pro Gln Met Cys Gln Arg Val Ser Glu Ile Glu Pro Arg
 1 5 10 15
 Thr Gln Phe Phe Asn Arg Cys Ala Leu Pro His Tyr Trp His Phe Pro
 20 25 30
 Ala Val Ala Val Phe Ser Lys His Ala Ser Leu Asp Glu Leu Ala Pro

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| | | |
|---|-----|-------------|
| 35 | 40 | 45 |
| Arg Asn Pro Arg Arg Ser Ser Arg Arg Asp Ala Glu Asp Arg Arg Val | | |
| 50 | 55 | 60 |
| Ile Phe Ala Ala Thr Leu Val Ala Val Asp Pro Pro Leu Arg Gly Ala | | |
| 65 | 70 | 75 80 |
| Gly Gly Glu Ala Asp Gln Leu Ile Asp Leu Gly Val Cys Arg Arg Gln | | |
| | 85 | 90 95 |
| Ala Gly Arg Val Arg Arg Gly Gln Glu Leu His His Arg His Arg His | | |
| | 100 | 105 110 |
| Gln Gly Ala Ala Pro Asp Leu Arg Arg Arg Arg Arg His Arg Arg Val | | |
| | 115 | 120 125 |
| Gln Gln His Arg Arg Leu Gln Arg Val Arg Gln Leu Arg Arg Tyr Val | | |
| | 130 | 135 140 |
| Gln Thr Ala His His Arg Arg Phe Ala Arg Thr Asp Arg Val Arg His | | |
| | 145 | 150 155 160 |
| His Val Arg Gly Pro Ser Asn His Arg Arg Arg Arg Val Tyr Arg Gly | | |
| | 165 | 170 175 |
| Arg His Ser Gly Ala Gly Gly Cys Pro Ala Gly Gly Ala Gly Ser Val | | |
| | 180 | 185 190 |
| Gly Gly Ser Ala | | |
| | 195 | |

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

| |
|---|
| Val Arg Cys Gly Thr Leu Val Pro Val Pro Met Val Glu Phe Leu Thr |
| 1 5 10 15 |
| Ser Thr Asn Ala Pro Ser Leu Pro Ser Ala Tyr Ala Glu Val Asp Lys |
| 20 25 30 |
| Leu Ile Gly Leu Pro Ala Gly Thr Ala Lys Arg Trp Ile Asn Gly Tyr |
| 35 40 45 |
| Glu Arg Gly Gly Lys Asp His Pro Pro Ile Leu Arg Val Thr Pro Gly |
| 50 55 60 |
| Ala Thr Pro Trp Val Thr Trp Gly Glu Phe Val Glu Thr Arg Met Leu |

65 70 75 80
 Ala Glu Tyr Arg Asp Arg Arg Lys Val Pro Ile Val Arg Gln Arg Ala
 85 90 95
 Ala Ile Glu Glu Leu Arg Ala Arg Phe Asn Leu Arg Tyr Pro Leu Ala
 100 105 110
 His Leu Arg Pro Phe Leu Ser Thr His Glu Arg Asp Leu Thr Met Gly
 115 120 125
 Gly Glu Glu Ile Gly Leu Pro Asp Ala Glu Val Thr Ile Arg Thr Gly
 130 135 140
 Gln Ala Leu Leu Gly Asp Ala Arg Trp Leu Ala Ser Leu Val Pro Asn
 145 150 155 160
 Ser Ala Arg Gly Ala Thr Leu Arg Arg Leu Gly Ile Thr Asp Val Ala
 165 170 175
 Asp Leu Arg Ser Ser Arg Glu Val Ala Arg Arg Gly Pro Gly Arg Val
 180 185 190
 Pro Asp Gly Ile Asp Val His Leu Leu Pro Phe Pro Asp Leu Ala Asp
 195 200 205
 Asp Asp Ala Asp Asp Ser Ala Pro His Glu Thr Ala Phe Lys Arg Leu
 210 215 220
 Leu Thr Asn Asp Gly Ser Asn Gly Glu Ser Gly Glu Ser Ser Gln Ser
 225 230 235 240
 Ile Asn Asp Ala Ala Thr Arg Tyr Met Thr Asp Glu Tyr Arg Gln Phe
 245 250 255
 Pro Thr Arg Asn Gly Ala Gln Arg Ala Leu His Arg Val Val Thr Leu
 260 265 270
 Leu Ala Ala Gly Arg Pro Val Leu Thr His Cys Phe Ala Gly Lys Asp
 275 280 285
 Arg Thr Gly Phe Val Val Ala Leu Val Leu Glu Ala Val Gly Leu Asp
 290 295 300
 Arg Asp Val Ile Val Ala Asp
 305 310

(2) INFORMATION FOR SEQ ID NO:189:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2072 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

| | |
|--|------|
| CTCGTGCCGA TTCGGCACGA GCTGAGCAGC CCAAGGGGCC GTTCGGCGAA GTCATCGAGG | 60 |
| CATTCGCCGA CGGGCTGGCC GGCAAGGGTA AGCAAATCAA CACCACGCTG AACAGCCTGT | 120 |
| CGCAGGCGTT GAACGCCTTG AATGAGGGCC GCGGCGACTT CTTGCGGGTG GTACGCAGCC | 180 |
| TGGCGCTATT CGTCAACGCG CTACATCAGG ACGACCAACA GTTCGTCGCG TTGAACAAGA | 240 |
| ACCTTGCGGA GTTCACCGAC AGGTGACCC ACTCCGATGC GGACCTGTCG AACGCCATCC | 300 |
| AGCAATTCGA CAGCTTGCTC GCCGTCGCGC GCCCGTTCTT CGCCAAGAAC CGCGAGGTGC | 360 |
| TGACGCATGA CGTCAATAAT CTCGCGACCG TGACCACCAC GTTGCTGCAG CCCGATCCGT | 420 |
| TGGATGGGTT GGAGACCGTC CTGCACATCT TCCCGACGCT GGCGGCGAAC ATTAACCAGC | 480 |
| TTTACCATCC GACACACGGT GGCGTGGTGT CGCTTTCCGC GTTCACGAAT TTCGCCAACC | 540 |
| CGATGGAGTT CATCTGCAGC TCGATTCAGG CGGGTAGCCG GCTCGGTTAT CAAGAGTCGG | 600 |
| CCGAACTCTG TGCAGTAT CTGGCGCCAG TCCTCGATGC GATCAAGTTC AACTACTTTC | 660 |
| CGTTTCGGCCT GAACGTGGCC AGCACCGCCT CGACACTGCC TAAAGAGATC GCGTACTCCG | 720 |
| AGCCCCGCTT GCAGCCGCCC AACGGGTACA AGGACACCAC GGTGCCCAGC ATCTGGGTGC | 780 |
| CGGATACGCC GTTGTACAC CGCAACACGC AGCCCCGTTG GGTGGTGGCA CCCGGGATGC | 840 |
| AAGGGGTTCA GGTGGGACCG ATCACGCAGG GTTTGCTGAC GCCGGAGTCC CTGGCCGAAC | 900 |
| TCATGGGTGG TCCCGATATC GCCCTCCGT CGTCAGGGCT GCAAACCCCG CCCGGACCCC | 960 |
| CGAATGCGTA CGACGAGTAC CCCGTGCTGC CGCCGATCGG TTTACAGGCC CCACAGGTGC | 1020 |
| CGATACCACC GCCGCCTCCT GGGCCCGACG TAATCCCCGG TCCGGTGCCA CCGGTCTTGG | 1080 |
| CGGCGATCGT GTTCCCAAGA GATCGCCCGG CAGCGTCGGA AAACCTCGAC TACATGGGCC | 1140 |
| TCTTGTTGCT GTCGCCGGGC CTGGCGACCT TCCTGTTCCG GGTGTCATCT AGCCCCGCCC | 1200 |
| GTGGAACGAT GGCCGATCGG CACGTGTTGA TACCGGCGAT CACCGGCCTG GCGTTGATCG | 1260 |
| CGGCATTCTG CGCACATTCG TGGTACCGCA CAGAACATCC GCTCATAGAC ATGCGCTTGT | 1320 |
| TCCAGAACCG AGCGGTCGCG CAGGCCAACA TGACGATGAC GGTGCTCTCC CTCGGGCTGT | 1380 |
| TTGGCTCCTT CTTGCTGCTC CCGAGCTACC TCCAGCAAGT GTTGACACAA TCACCGATGC | 1440 |
| AATCGGGGGT GCATATCATC CCACAGGGCC TCGGTGCCAT GCTGGCGATG CCGATCGCCG | 1500 |
| GAGCGATGAT GGACCGACGG GGACCGGCCA AGATCGTGCT GGTGGGATC ATGCTGATCG | 1560 |
| CTGCGGGGTT GGGCACCTTC GCCTTTGGTG TCGCGCGGCA AGCGGACTAC TTACCCATTC | 1620 |

TGCCGACCGG GCTGGCAATC ATGGGCATGG GCATGGGCTG CTCCATGATG CCACTGTCCG 1680
 GGGCGGCAGT GCAGACCCTG GCCCCACATC AGATCGCTCG CGGTTTCGACG CTGATCAGCG 1740
 TCAACCAGCA GGTGGGCGGT TCGATAGGGA CCGCACTGAT GTCGGTGCTG CTCACCTACC 1800
 AGTTCAATCA CAGCGAAATC ATCGCTACTG CAAAGAAAGT CGCACTGACC CCAGAGAGTG 1860
 GCGCCGGGCG GGGGGCGGCG GTTGACCCCTT CCTCGCTACC GCGCCAAACC AACTTCGCGG 1920
 CCCAACTGCT GCATGACCTT TCGCACGCCT ACGCGGTGGT ATTCGTGATA GCGACCGCGC 1980
 TAGTGGTCTC GACGCTGATC CCCGCGGCAT TCCTGCCGAA ACAGCAGGCT AGTCATCGAA 2040
 GAGCACCGTT GCTATCCGCA TGACGTCTGC TT 2072

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1923 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TCACCCCGGA GAAGTCGTTT GTCGACGACC TGGACATCGA CTCGCTGTCTG ATGGTCGAGA 60
 TCGCCGTGCA GACCGAGGAC AAGTACGGCG TCAAGATCCC CGACGAGGAC CTCGCCGGTC 120
 TGCCTACCGT CGGTGACGTT GTCGCCTACA TCCAGAAGCT CGAGGAAGAA AACCCGGAGG 180
 CGGCTCAGGC GTTGCGCGCG AAGATTGAGT CGGAGAACCC CGATGCGGCA CGAGCAGATC 240
 GGTGCGTTTC ACCCACATCG CAAGCTCGAG ACGCCCGTCG TCCTCTTGCA CGCTCAGCCA 300
 GGTGCGGTG TCGCCGCCTT CCAGCAAGTG TTCCACCAC ACGAAGGGAC CCTCGCGAAA 360
 GGTGACTGAT CCGCGGACCA CATAGTCGAT GCCACCGTGG CTGACAATTG CGCCGGGTCC 420
 GAGTTGGCGG GGGCCGAATT GCGGCATTGC GTCGAAGGCC AGCGGATCCC GGCGCCCGCC 480
 CGGCGTGGCT GGTGTTTTTG GCCCGCGGAT GGCCACGACG AGAACGACGA TGGCGGCGAT 540
 GAACAGCGCC ACGGCAATCA CGACCAGCAG ATTTCCACG CATACCTCT CTACCGCTG 600
 CGCCGCGGTT GGTGATCGG TCGCATATCG ATGGCGCCGT TTAACGTAAC AGCTTTCGCG 660
 GGACCGGGGG TCACAACGGG CGAGTTGTCC GGCCGGGAAC CCGGCAGGTC TCGGCCGCGG 720
 TCACCCAGC TCACTGGTGC ACCATCCGGG TGTCGGTGAG CGTGCAACTC AAACACACTC 780
 AACGGCAACG GTTTCTCAGG TCACCAGCTC AACCTCGACC CGCAATCGCT CGTACGTTTC 840

GACCGCGCGC AGGTCGCGAG TCAGCAGCTT TGCGCCGGCA GCTTTCGCCG TGAAGCCGAC 900
 CAGGGCATCG TAGGTTGCGC CACCGGTGAC ATCGTGCTCG GCGAGGTGGT CCGTCAAGCC 960
 GCGATATGAG CAGGCATCCA GTGCCAGGTA GTTGCTGGAG GTGATGTCCG CCAAGTAGGC 1020
 GTGGACGGCA ACAGGGGCAA TACGATGCGG CGGTGGTAGC CGGGTCAAGA CCGAATAGGT 1080
 TTCCACAGCC GCGTGCGCGA TCAGATGGAC GCCACGGTTG AGCGCGCGCA CGGCGGCCTC 1140
 GTGCCCTTCG TGCCAGGTCG CGAATCCGGC AACCAGCACG CTGGTGCTCG GTGCGATCAC 1200
 CGCCGTGTGC GATCGAGCGT TTCCCGAACG ATTTCTGTCG TCAACGGGGG CAGGGGACGT 1260
 TCTGGCCGTG CGACGAGAAC CGAGCCTTCC CGAACGAGTT CGACACCGGT CGGGGCCGGC 1320
 TCAATCTCGA TGCGCCCATC GCGCTCGGTG ATCTCCACCT GGTCGTTCCC GCGCAAGCCA 1380
 AGGCGCTCGC GAATCCGCTT GGAATCACC AGACGTCTCG CGACATCGAT GGTGTTCGC 1440
 ATGGTAGGAA ATTTACCATC GCACGTTCCA TAGGCGTGTC CTGCGCGGGA TGTCGGGACG 1500
 ATCCGCTAGC GTATCGAACG ATTGTTTCGG AAATGGCTGA GGGAGCGTGC GGTGCGGGTG 1560
 ATGGGTGTGC ATCCCGGGTT GACCCGATGC GGGCTGTGCG TCATCGAGAG TGGGCGTGGT 1620
 CGGCAGCTCA CCGCGCTGGA TGTCGACGTG GTGCGCACAC CGTCGGATGC GGCCTTGGCG 1680
 CAGCGCCTGT TGGCCATCAG CGATGCCGTC GAGCACTGGC TGGACACCCA TCATCCGGAG 1740
 GTGGTGGCTA TCGAACGGGT GTTCTCTCAG CTCAACGTGA CCACGGTGAT GGGCACCGCG 1800
 CAGGCCGGCG GCGTGATCGC CCTGGCGGCG GCCAAACGTG GTGTCGACGT GCATTTCCAT 1860
 ACCCCCAGCG AGGTCAAGGC GCGGGTCACT GGCAACGGTT CCGCAGACAA GGCTCAGGTC 1920
 ACC 1923

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1055 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

CTGGCGTGCC AGTGTCACCG GCGATATGAC GTCGGCATTG AATTTCGCGG CCCC GCCGGA 60
 CCCGTCGCCA CCCAATCTGG ACCACCCGGT CCGTCAATTG CCGAAGGTCG CCAAGTGCGT 120
 GCCCAATGTG GTGCTGGGTT TCTTGAACGA AGGCCTGCCG TATCGGGTGC CCTACCCCCA 180
 AACAAACGCCA GTCCAGGAAT CCGGTCCCGC GCGGCCGATT CCCAGCGGCA TCTGCTAGCC 240

GGGGATGGTT CAGACGTAAC GGTTGGCTAG GTCGAAACCC GCGCCAGGGC CGCTGGACGG 300
 GCTCATGGCA GCGAAATTAG AAAACCCGGG ATATTGTCCG CGGATTGTCA TACGATGCTG 360
 AGTGCTTGGT GGTTCTGTGT TAGCCATTGA GTGTGGATGT GTTGAGACCC TGGCCTGGAA 420
 GGGGACAACG TGCTTTTGCC TCTTGGTCCG CCTTTGCCGC CCGACGCGGT GGTGGCGAAA 480
 CGGGCTGAGT CGGGAATGCT CGGCGGGTTG TCGGTTCCGC TCAGCTGGGG AGTGGCTGTG 540
 CCACCCGATG ATTATGACCA CTGGGCGCCT GCGCCGGAGG ACGGCGCCGA TGTCGATGTC 600
 CAGGCGGCCG AAGGGGCGGA CGCAGAGGCC GCGGCCATGG ACGAGTGGGA TGAGTGGCAG 660
 GCGTGGAACG AGTGGGTGGC GGAGAACGCT GAACCCCGCT TTAGGTGCC ACGGAGTAGC 720
 AGCAGCGTGA TTCCGCATTC TCCGGCGGCC GGCTAGGAGA GGGGGCGCAG ACTGTCGTTA 780
 TTTGACCAGT GATCGGCGGT CTCGGTGTTT CCGCGGCCGG CTATGACAAC AGTCAATGTG 840
 CATGACAAGT TACAGGTATT AGGTCCAGGT TCAACAAGGA GACAGGCAAC ATGGCAACAC 900
 GTTTTATGAC GGATCCGCAC GCGATGCGGG ACATGGCGGG CCGTTTTGAG GTGCACGCCC 960
 AGACGGTGGA GGACGAGGCT CGCCGATGT GGGCGTCCGC GCAAAACATC TCGGGNGCGG 1020
 GCTGGAGTGG CATGGCCGAG GCGACCTCGC TAGAC 1055

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

CCGCCTCGTT GTTGGCATA TCCGCCGCGG CCGCCTCGAC CGCACTGGCC GTGGCGTGTG 60
 TCCGGGCTGA CCACCGGGAT CGCCGAACCA TCCGAGATCA CCTCGCAATG ATCCACCTCG 120
 CGCAGCTGGT CACCCAGCCA CCGGGCGGTG TCGCAGACG CCTGCATCAC CTTGGTATAG 180
 CCGTCGCGCC CCAGCCGCGAG GAAGTTGTAG TACTGGCCCA CCACCTGGTT ACCGGGACGG 240
 GAGAAGTTCA GGGTGAAGGT CGGCATGTCG CCGCCGAGGT AGTTGACCCG GAAAACCAGA 300
 TCCTCCGGCA GGTGCTCGGG CCCGCGCCAC ACGACAAACC CGACGCCGGG ATAGGTCAG 359

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

```

AACGGGCCCCG TGGGCACCGC TCCTCTAAGG GCTCTCGTTG GTCGCATGAA GTGCTGGAAG      60
GATGCATCTTT GGCAGATTCC CGCCAGAGCA AACAGCCGC TAGTCCTAGT CCGAGTCGCC      120
CGCAAAGTTC CTCGAATAAC TCCGTACCCG GAGCGCCAAA CCGGGTCTCC TTCGCTAAGC      180
TGCGCGAACC ACTTGAGGTT CCGGGACTCC TTGACGTCCA GACCGATTCTG TTCGAGTGGC      240
TGATCGGTTTC GCCGCGCTGG CGCGAATCCG CCGCCGAGCG GGGTGATGTC AACCCAGTGG      300
GTGGCCTGGA AGAGGTGCTC TACGAGCTGT CTCCGATCGA GGACTTCTCC      350
  
```

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```

Glu Gln Pro Lys Gly Pro Phe Gly Glu Val Ile Glu Ala Phe Ala Asp
1           5           10           15

Gly Leu Ala Gly Lys Gly Lys Gln Ile Asn Thr Thr Leu Asn Ser Leu
20          25          30

Ser Gln Ala Leu Asn Ala Leu Asn Glu Gly Arg Gly Asp Phe Phe Ala
35          40          45

Val Val Arg Ser Leu Ala Leu Phe Val Asn Ala Leu His Gln Asp Asp
50          55          60

Gln Gln Phe Val Ala Leu Asn Lys Asn Leu Ala Glu Phe Thr Asp Arg
65          70          75          80

Leu Thr His Ser Asp Ala Asp Leu Ser Asn Ala Ile Gln Gln Phe Asp
85          90          95

Ser Leu Leu Ala Val Ala Arg Pro Phe Phe Ala Lys Asn Arg Glu Val
100         105         110

Leu Thr His Asp Val Asn Asn Leu Ala Thr Val Thr Thr Leu Leu
115         120         125

Gln Pro Asp Pro Leu Asp Gly Leu Glu Thr Val Leu His Ile Phe Pro
130         135         140
  
```

209220 CH848001

Thr Leu Ala Ala Asn Ile Asn Gln Leu Tyr His Pro Thr His Gly Gly
 145 150 155 160
 Val Val Ser Leu Ser Ala Phe Thr Asn Phe Ala Asn Pro Met Glu Phe
 165 170 175
 Ile Cys Ser Ser Ile Gln Ala Gly Ser Arg Leu Gly Tyr Gln Glu Ser
 180 185 190
 Ala Glu Leu Cys Ala Gln Tyr Leu Ala Pro Val Leu Asp Ala Ile Lys
 195 200 205
 Phe Asn Tyr Phe Pro Phe Gly Leu Asn Val Ala Ser Thr Ala Ser Thr
 210 215 220
 Leu Pro Lys Glu Ile Ala Tyr Ser Glu Pro Arg Leu Gln Pro Pro Asn
 225 230 235 240
 Gly Tyr Lys Asp Thr Thr Val Pro Gly Ile Trp Val Pro Asp Thr Pro
 245 250 255
 Leu Ser His Arg Asn Thr Gln Pro Gly Trp Val Val Ala Pro Gly Met
 260 265 270
 Gln Gly Val Gln Val Gly Pro Ile Thr Gln Gly Leu Leu Thr Pro Glu
 275 280 285
 Ser Leu Ala Glu Leu Met Gly Gly Pro Asp Ile Ala Pro Pro Ser Ser
 290 295 300
 Gly Leu Gln Thr Pro Pro Gly Pro Pro Asn Ala Tyr Asp Glu Tyr Pro
 305 310 315 320
 Val Leu Pro Pro Ile Gly Leu Gln Ala Pro Gln Val Pro Ile Pro Pro
 325 330 335
 Pro Pro Pro Gly Pro Asp Val Ile Pro Gly Pro Val Pro Pro Val Leu
 340 345 350
 Ala Ala Ile Val Phe Pro Arg Asp Arg Pro Ala Ala Ser Glu Asn Phe
 355 360 365
 Asp Tyr Met Gly Leu Leu Leu Leu Ser Pro Gly Leu Ala Thr Phe Leu
 370 375 380
 Phe Gly Val Ser Ser Ser Pro Ala Arg Gly Thr Met Ala Asp Arg His
 385 390 395 400
 Val Leu Ile Pro Ala Ile Thr Gly Leu Ala Leu Ile Ala Ala Phe Val
 405 410 415
 Ala His Ser Trp Tyr Arg Thr Glu His Pro Leu Ile Asp Met Arg Leu
 420 425 430
 Phe Gln Asn Arg Ala Val Ala Gln Ala Asn Met Thr Met Thr Val Leu

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| | | |
|-------------------------|-----------------------------|-----------------|
| 435 | 440 | 445 |
| Ser Leu Gly Leu Phe Gly | Ser Phe Leu Leu Leu Pro | Ser Tyr Leu Gln |
| 450 | 455 | 460 |
| Gln Val Leu His Gln Ser | Pro Met Gln Ser Gly Val His | Ile Ile Pro |
| 465 | 470 | 475 |
| Gln Gly Leu Gly Ala Met | Leu Ala Met Pro Ile Ala Gly | Ala Met Met |
| 485 | 490 | 495 |
| Asp Arg Arg Gly Pro Ala | Lys Ile Val Leu Val Gly | Ile Met Leu Ile |
| 500 | 505 | 510 |
| Ala Ala Gly Leu Gly Thr | Phe Ala Phe Gly Val Ala Arg | Gln Ala Asp |
| 515 | 520 | 525 |
| Tyr Leu Pro Ile Leu Pro | Thr Gly Leu Ala Ile Met | Gly Met Gly Met |
| 530 | 535 | 540 |
| Gly Cys Ser Met Met Pro | Leu Ser Gly Ala Ala Val | Gln Thr Leu Ala |
| 545 | 550 | 555 |
| Pro His Gln Ile Ala Arg | Gly Ser Thr Leu Ile Ser | Val Asn Gln Gln |
| 565 | 570 | 575 |
| Val Gly Gly Ser Ile Gly | Thr Ala Leu Met Ser Val | Leu Leu Thr Tyr |
| 580 | 585 | 590 |
| Gln Phe Asn His Ser Glu | Ile Ile Ala Thr Ala Lys | Lys Val Ala Leu |
| 595 | 600 | 605 |
| Thr Pro Glu Ser Gly Ala | Gly Arg Gly Ala Ala Val | Asp Pro Ser Ser |
| 610 | 615 | 620 |
| Leu Pro Arg Gln Thr Asn | Phe Ala Ala Gln Leu Leu | His Asp Leu Ser |
| 625 | 630 | 635 |
| His Ala Tyr Ala Val Val | Phe Val Ile Ala Thr Ala | Leu Val Val Ser |
| 645 | 650 | 655 |
| Thr Leu Ile Pro Ala Ala | Phe Leu Pro Lys Gln Gln | Ala Ser His Arg |
| 660 | 665 | 670 |
| Arg Ala Pro Leu Leu Ser | Ala | |
| 675 | | |

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

1008443.02503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Thr Pro Glu Lys Ser Phe Val Asp Asp Leu Asp Ile Asp Ser Leu Ser
 1 5 10 15
 Met Val Glu Ile Ala Val Gln Thr Glu Asp Lys Tyr Gly Val Lys Ile
 20 25 30
 Pro Asp Glu Asp Leu Ala Gly Leu Arg Thr Val Gly Asp Val Val Ala
 35 40 45
 Tyr Ile Gln Lys Leu Glu Glu Glu Asn Pro Glu Ala Ala Gln Ala Leu
 50 55 60
 Arg Ala Lys Ile Glu Ser Glu Asn Pro Asp Ala Ala Arg Ala Asp Arg
 65 70 75 80
 Cys Val Ser Pro Thr Ser Gln Ala Arg Asp Ala Arg Arg Pro Leu Ala
 85 90 95
 Arg Ser Ala Arg Leu Ala Cys Arg Arg Leu Pro Ala Ser Val Pro Thr
 100 105 110
 Thr Arg Arg Asp Pro Arg Glu Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Leu Ala Cys Gln Cys His Arg Arg Tyr Asp Val Gly Ile Gln Phe Arg
 1 5 10 15
 Gly Pro Ala Gly Pro Val Ala Thr Gln Ser Gly Pro Pro Gly Pro Ser
 20 25 30
 Ile Ala Glu Gly Arg Gln Val Arg Ala Gln Cys Gly Ala Gly Phe Leu
 35 40 45
 Glu Arg Arg Pro Ala Val Ser Gly Ala Leu Pro Pro Asn Asn Ala Ser
 50 55 60
 Pro Gly Ile Arg Ser Arg Ala Ala Asp Ser Gln Arg His Leu Leu Ala
 65 70 75 80
 Gly Asp Gly Ser Asp Val Thr Val Gly
 85

(2) INFORMATION FOR SEQ ID NO:197:

205220"248800T

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Ala Ser Leu Leu Ala Tyr Ser Ala Ala Ala Ser Thr Ala Leu Ala
 1 5 10 15

Val Ala Cys Val Arg Ala Asp His Arg Asp Arg Arg Thr Ile Arg Asp
 20 25 30

His Leu Ala Met Ile His Leu Ala Gln Leu Val Thr Gln Pro Pro Gly
 35 40 45

Gly Val Arg Gln Arg Leu His His Leu Gly Ile Ala Val Ala Pro Gln
 50 55 60

Pro Gln Glu Val Val Val Leu Ala His His Leu Val Thr Gly Thr Gly
 65 70 75 80

Glu Val Gln Gly Glu Gly Arg His Val Ala Ala Glu Val Val Asp Pro
 85 90 95

Glu Asn Gln Ile Leu Arg Gln Val Leu Gly Pro Ala Pro His Asp Lys
 100 105 110

Pro Asp Ala Gly Ile Gly Gln
 115

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Arg Ala Arg Gly His Arg Ser Ser Lys Gly Ser Arg Trp Ser His Glu
 1 5 10 15

Val Leu Glu Gly Cys Ile Leu Ala Asp Ser Arg Gln Ser Lys Thr Ala
 20 25 30

Ala Ser Pro Ser Pro Ser Arg Pro Gln Ser Ser Ser Asn Asn Ser Val
 35 40 45

Pro Gly Ala Pro Asn Arg Val Ser Phe Ala Lys Leu Arg Glu Pro Leu
 50 55 60

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 205220" E4B4800T

Glu Val Pro Gly Leu Leu Asp Val Gln Thr Asp Ser Phe Glu Trp Leu
65 70 75 80

Ile Gly Ser Pro Arg Trp Arg Glu Ser Ala Ala Glu Arg Gly Asp Val
85 90 95

Asn Pro Val Gly Gly Leu Glu Glu Val Leu Tyr Glu Leu Ser Pro Ile
100 105 110

Glu Asp Phe Ser
115

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 811 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

| | |
|--|-----|
| TGCTACGCAG CAATCGCTTT GGTGACAGAT GTGGATGCCG GCGTCGCTGC TGGCGATGGC | 60 |
| GTGAAAGCCG CCGACGTGTT CGCCGCATTC GGGGAGAACA TCGAACTGCT CAAAAGGCTG | 120 |
| GTGCGGGCCG CCATCGATCG GGTCGCCGAC GAGCGCACGT GCACGCACTG TCAACACCAC | 180 |
| GCCGGTGTTT CGTTGCCGTT CGAGCTGCCA TGAGGGTGCT GCTGACCGGC GCGGCCGGCT | 240 |
| TCATCGGGTC GCGCGTGGAT GCGGCGTTAC GGGCTGCGGG TCACGACGTG GTGGGCGTCG | 300 |
| ACGCGCTGCT GCCCGCCGCG CACGGGCCAA ACCCGGTGCT GCCACCGGGC TGCCAGCGGG | 360 |
| TCGACGTGCG CGACGCCAGC GCGCTGGCCC CGTTGTTGGC CGGTGTCGAT CTGGTGTGTC | 420 |
| ACCAGGCCGC CATGGTGGGT GCCGGCGTCA ACGCCGCCGA CGCACC CGCC TATGGCGGCC | 480 |
| ACAACGATTT CGCCACCACG GTGCTGCTGG CGCAGATGTT CGCCGCCGGG GTCCGCCGTT | 540 |
| TGGTGCTGGC GTCGTCGATG GTGGTTTACG GGCAGGGGCG CTATGACTGT CCCCAGCATG | 600 |
| GACCGGTCGA CCCGCTGCCG CGGCGGCGAG CCGACCTGGA CAATGGGGTC TTCGAGCACC | 660 |
| GTTGCCCGGG GTGCGGCGAG CCAGTCATCT GGCAATTGGT CGACGAAGAT GCCCCGTTGC | 720 |
| GCCCGCGCAG CCTGTACGCG GCAGCAAGAC CGCGCAGGAG CACTACGCGC TGGCGTGGTC | 780 |
| GGAAACGAAT GGCGGTTCCG TGGTGGCGTT G | 811 |

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 966 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

| | |
|---|-----|
| GTCCCGCGAT GTGGCCGAGC ATGACTTTTCG GCAACACCCGG CGTAGTAGTC GAAGATATCG | 60 |
| GACTTTGTGG TCCCGGTGGC GGGATAGAGC ACCTGTCGGC GTTGGTCAGC GTCACCCGTT | 120 |
| GCTCGGACGC CGAACCCATG CTTTCAACGT AGCCTGTCGG TCACACAAGT CGCGAGCGTA | 180 |
| ACGTCACGGT CAAATATCGC GTGGAATTTT GCCGTGACGT TCCGCTCGCG GACAATCAAG | 240 |
| GCATACTCAC TTACATGCGA GCCATTTGGA CGGGTTCGAT CGCCTTCGGG CTGGTGAACG | 300 |
| TGCCGGTCAA GGTGTACAGC GCTACCGCAG ACCACGACAT CAGGTTCCAC CAGGTGCACG | 360 |
| CCAAGGACAA CGGACGCATC CGGTACAAGC GCGTCTGCGA GGCGTGTGGC GAGGTGGTCG | 420 |
| ACTACCGCGA TCTTGCCCGG GCCTACGAGT CCGGCGACGG CCAAATGGTG GCGATCACCG | 480 |
| ACGACGACAT CGCCAGCTTG CCTGAAGAAC GCAGCCGGGA GATCGAGGTG TTGGAGTTTCG | 540 |
| TCCCCGCCGC CGACGTGGAC CCGATGATGT TCGACCGCAG CTACTTTTTG GAGCCTGATT | 600 |
| CGAAGTCGTC GAAATCGTAT GTGCTGCTGG CTAAGACACT CGCCGAGACC GACCGGATGG | 660 |
| CGATCGTGGA TCGCCCCACC GGCCGTGAAT GCAGGAAAAA TAAGAGCCGC TATCCACAAT | 720 |
| TCGGCGTCGA GCTCGGCTAC CACAAACGGT AGAACGATCG AGACATTCCC GAGCTGAAGT | 780 |
| GCGGCGCTAT AGAAGCCGCT CTGCGCGATT ATCAAACGCA AAATACGCTT ACTCATGCCA | 840 |
| TCGGCGCTGC TCACCCGATG CGACGTTTTT GCCACGCTCC ACCGCCTGCC GCGCGACCTC | 900 |
| AAGTGGGCAT GCATCCCACC CGTTCCCGGA AACCGGTTCC GGCGGGTCGG CTCATCGCTT | 960 |
| CATCCT | 966 |

(2) INFORMATION FOR SEQ ID NO:201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

| | |
|--|-----|
| CCGCACCGCC GGCAATACCG CCAGCGCCAC CGTTACCGCC GTTTGCGCCG TTGCCCCCGT | 60 |
| TGCCGCCCCGT CCCGCCGGCC CCGCCGATGG AGTTCTCATC GCCAAAAGTA CTGGCGTTGC | 120 |
| CACCGGAGCC GCCGTTGCCG CCGTCACCGC CAGCCCCGCC GACTCCACCG GCCCCACCGA | 180 |

CTCCGCCGCT GCCACCGTTG CCGCCGTTGC CGATCAACAT GCCGCTGGCG CCACCCTTGC 240
 CACCCACGCC ACCGGCTCCG CCCACCCCGC CGACACCAAG CGAGCTGCCG CCGGAGCCAC 300
 CATCACCACC TACGCCACCG ACCGCCCAGA CACCAGCGAC CGGGTCTTCG TGAAACGTCTG 360
 CGGTGCCACC ACCGCCGCCG TTACCGCCAA CCCACCGGC AACGCCGGCG CCGCCATCCC 420
 CGCCGGCCCC GGC GTTGCCG CCGTTGCCGC CGTTGCCGAA CAACAACCCG CCGGCGCCGC 480
 CGTTGCCGCC CGCGCCGCCG GTCCCGCCGG CGCCGCCGAC GCCAAGGCCG CTGCCGCCCT 540
 TGCCGCCATC ACCACCTTG CCGCCGACCA CATCGGGTTC TGCCTCGGGG TCTGGGCTGT 600
 CAAACCTCGC GATGCCAGCG TTGCCGCCGC TTCCCCCGGG CCCCCCGTG GCGCCGTCAC 660
 CACCGATACC ACCCGCGCCA CCGGCGCCAC CGTTGCCGCC ATCACC GAAT AGCAACCCGC 720
 CGGCGCCACC ATTGCCGCCA GTCCTCCCTG CGCCACCGTC GCGCGCCGAG GCGGCACTGG 780
 CAGCCCCGTT ACCACCGAAA CCGCCGCTAC CACCGGTAGA GGTGGCAGTG GCGATGTGTA 840
 CGAAAGCGCC GCCTCCGGCG CCGCCGCTAC CACCCCCACT GCCGGCGGCT ACACCGTCGG 900
 ACCCGTTGCC ACCATCACCG CCAAAGGCGC TCGCAATGTC GCCCTGCGCG ACTCCGCCGT 960
 CGCCGCCGTT GCCGCCGCCG CCACCGGCAG CGGCGGTACC GCCGTCACCA CCGGCACCGC 1020
 CGGTGGCCTT GCCCGAGCCT GCCGTCGCGG TGGCACCGTC GCCGCCGGTG CCACCGGTCTG 1080
 GCGTGCCGGC AGTGCCATGG CCGCCCGTGC CGCCGTCGCC GCCGTTTGA TCACCGATGC 1140
 CGGACACATC TGCCGGGCTG TCCCCGGTGC TGGCCGCGGG GCCGGGCGTG GGATTGACCC 1200
 CGTTTGCCCC GGCAGGGCCG GCGCCGCCGG TACCACCGGC GCCGCCATGG CCGAACAGCC 1260
 CGGCGTTGCC GCCGTTACCG CCCGCACCCC CGATGCCTGC GGCCACGCTG GTGCCGCCGA 1320
 CACCGCCGTT GCCGCCGTTG CCCACAACC ACCCCCCGTT CCCACCGGCA CCGCCGGCCG 1380
 CGCCGGTACC ACCGGCCCCG CCGTTGCCGC CGTTGCCGAT CAACCCGGCC GCGCCTCCGC 1440
 TGCCGCCGGT TTGACCGAAC CCGCCAGCCG CGCCGTTGCC ACCGTTGCCA AACAGCAACC 1500
 CGCCGGCCGC GCCAGGCTGC CCGGGTGCCG TCCCGTCGGC GCCGTTTCCG ATCAACGGGC 1560
 GCCCCAAAAG CGCCTCGGTG GCGCATTTCA CCGCACCCAG CAGACTCCGC TCAACAGCGG 1620
 CTTCAGTGCT GGCATACCGA CCCGCGGCCG CAGTCAACGC CTGCACAAAC TGCTCGTGAA 1680
 ACGCTGCCAC CTGTACGCTG AGCGCCTGAT ACTGCCGAGC ATGGGCCCCG AACAAACCCG 1740
 CAATCGCCGC CGACACTTCA TCGGCAGCCG CAGCCACCAC TTCCGTCGTC GGGATCGCCG 1800
 CGGCCGCATT AGCCGCGCTC ACCTGCGAAC CAATAGTCGA TAAATCCAAA GCCGCAGTTG 1860

CCAGCAGCTG CGGCGTCGCG ATCACCAAGG ACACCTCGCA CCTCCGGATA CCCCATATCG 1920
 CCGCACCGTG TCCCCAGCGG CCACGTGACC TTTGGTCGCT GGCTGGCGGC CCTGACTATG 1980
 GCCGCGACGG CCCTCGTTCT GATTGCCCCC GGCGCGCAGC TTGTTGCGCG AGTTGAAGAC 2040
 GGGAGGACAG GCCGAGCTTG GTGTAGACGT GGGTCAAGTG GGAATGCACG GTCCGCGGCG 2100
 AGATGAATAG GCGGACGCCG ATCTCCTTGT TGCTGAGTCC CTCACCGACC AGTAGAGCCA 2160
 CCTCAAGCTC TGTCGGTGTC AACGCGCCCC AGCCACTTGT CGGGCGTTTC CGTGCACCGC 2220
 GGCCTCGTTG CGCGTACGCG ATCGCCTCAT CGATCGATAA CGCAGTTCCT TCGGCCCAGG 2280
 CATCGTCGAA CTCGCTGTCA CCCATGGATT TTCGAAGGGT GGCTAGCGAC GAGTTACAGC 2340
 CCGCCTGGTA GATCCCGAAG CGGACCG 2367

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Gln Pro Ala Gly Ala Thr Ile Ala Ala Ser Ser Pro Cys Ala Thr Val
 1 5 10 15
 Gly Ala Gly Gly Gly Thr Gly Ser Pro Val Thr Thr Glu Thr Ala Ala
 20 25 30
 Thr Thr Gly Arg Gly Gly Ser Gly Asp Val Tyr Glu Ser Ala Ala Ser
 35 40 45
 Gly Ala Ala Ala Thr Thr Pro Thr Ala Gly Gly Tyr Thr Val Gly Pro
 50 55 60
 Val Ala Thr Ile Thr Ala Lys Gly Ala Arg Asn Val Ala Leu Arg Asp
 65 70 75 80
 Ser Ala Val Ala Ala Val Ala Ala Ala Thr Gly Ser Gly Gly Thr
 85 90 95
 Ala Val Thr Thr Gly Thr Ala Gly Gly Leu Ala Arg Ala Cys Arg Arg
 100 105 110
 Gly Gly Thr Val Ala Ala Gly Ala Thr Gly Arg Arg Ala Gly Ser Ala
 115 120 125
 Met Ala Ala Arg Ala Ala Val Ala Ala Gly Leu Ile Thr Asp Ala Gly
 130 135 140

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His Ile Cys Arg Ala Val Pro Gly Ala Gly Arg Gly Ala Gly Arg Gly
 145 150 155 160
 Ile Asp Pro Val Cys Pro Gly Glu Ala Gly Ala Ala Gly Thr Thr Gly
 165 170 175
 Ala Ala Met Ala Glu Gln Pro Gly Val Ala Ala Val Thr Ala Arg Thr
 180 185 190
 Pro Asp Ala Cys Gly His Ala Gly Ala Ala Asp Thr Ala Val Ala Ala
 195 200 205
 Val Ala Pro Gln Pro Pro Pro Val Pro Thr Gly Thr Ala Gly Arg Ala
 210 215 220
 Gly Thr Thr Gly Pro Ala Val Ala Ala Val Ala Asp Gln Pro Gly Arg
 225 230 235 240
 Ala Ser Ala Ala Ala Gly Leu Thr Glu Pro Ala Ser Arg Ala Val Ala
 245 250 255
 Thr Val Ala Lys Gln Gln Pro Ala Gly Arg Ala Arg Leu Pro Gly Cys
 260 265 270
 Arg Pro Val Gly Ala Val Ser Asp Gln Arg Ala Pro Gln Lys Arg Leu
 275 280 285
 Gly Gly Arg Ile His Arg Thr Gln Gln Thr Pro Leu Asn Ser Gly Phe
 290 295 300
 Ser Ala Gly Ile Pro Thr Arg Gly Arg Ser Gln Arg Leu His Lys Leu
 305 310 315 320
 Leu Val Lys Arg Cys His Leu Tyr Ala Glu Arg Leu Ile Leu Pro Ser
 325 330 335
 Met Gly Pro Glu Gln Pro Arg Asn Arg Arg Arg His Phe Ile Gly Ser
 340 345 350
 Arg Ser His His Phe Arg Arg Arg Asp Arg Arg Gly Arg Ile Ser Arg
 355 360 365
 Ala His Leu Arg Thr Asn Ser Arg
 370 375

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

| | | | | | | |
|------------|-------------|-------------|-------------|------------|-------------|------|
| GGCCAAAACG | CCCCGGCGAT | CGCGGCCACC | GAGGCCGCCT | ACGACCAGAT | GTGGGCCCAG | 60 |
| GACGTGGCGG | CGATGTTTGG | CTACCATGCC | GGGGCTTCGG | CGGCCGTCTC | GGCGTTGACA | 120 |
| CCGTTCGGCC | AGGCGCTGCC | GACCGTGGCG | GGCGGCGGTG | CGCTGGTCAG | CGCGGCCCGG | 180 |
| GCTCAGGTGA | CCACGCGGGT | CTTCCGCAAC | CTGGGCTTGG | CGAACGTCCG | CGAGGGCAAC | 240 |
| GTCCGCAACG | GTAATGTCCG | GAAC TTCAAT | CTCGGCTCGG | CCAACATCGG | CAACGGCAAC | 300 |
| ATCGGCAGCG | GCAACATCGG | CAGCTCCAAC | ATCGGGTTTG | GCAACGTGGG | TCCTGGGTTG | 360 |
| ACCGCAGCGC | TGAACAACAT | CGGTTTCGGC | AACACCGGCA | GCAACAACAT | CGGGTTTGGC | 420 |
| AACACCGGCA | GCAACAACAT | CGGGTTTCGGC | AATACCGGAG | ACGGCAACCG | AGGTATCGGG | 480 |
| CTCACGGGTA | GCGGTTTGTT | GGGGTTTCGGC | GGCCTGAACT | CGGGCACCGG | CAACATCGGT | 540 |
| CTGTTCAACT | CGGGCACCGG | AAACGTCGGC | ATCGGCAACT | CGGGTACCGG | GAAC TTGGGC | 600 |
| ATTGGCAACT | CGGGCAACAG | CTACAACACC | GGTTTTGGCA | ACTCCGGCGA | CGCCAACACG | 660 |
| GGCTTCTTCA | ACTCCGGAAT | AGCCAACACC | GGCGTCGGCA | ACGCCGGCAA | CTACAACACC | 720 |
| GGTAGCTACA | ACCCGGGCAA | CAGCAATACC | GGCGGCTTCA | ACATGGGCCA | GTACAACACG | 780 |
| GGCTACCTGA | ACAGCGGCAA | CTACAACACC | GGCTTG GCAA | ACTCCGGCAA | TGTCAACACC | 840 |
| GGCGCCTTCA | TTACTGGCAA | CTTCAACAAC | GGCTTCTTGT | GGCGCGGCGA | CCACCAAGGC | 900 |
| CTGATTTTCG | GGAGCCCCGG | CTTCTTCAAC | TCGACCAGTG | CGCCGTCGTC | GGGATTCTTC | 960 |
| AACAGCGGTG | CCG GTAGCGC | GTCCGGCTTC | CTGAACTCCG | GTGCCAACAA | TTCTGGCTTC | 1020 |
| TTCAACTCTT | CGTCGGGGGC | CATCGGTAAC | TCCGGCCTGG | CAAACGCGGG | CGTGCTGGTA | 1080 |
| TCGGGCGTGA | TCAACTCGGG | CAACACCGTA | TCGGGTTTGT | TCAACATGAG | CCTGGTGGCC | 1140 |
| ATCACAACGC | CGGCCTTGAT | CTCGGGCTTC | TTCAACACCG | GAAGCAACAT | GTCGGGATTT | 1200 |
| TTCGGTGGCC | CACCGGTCTT | CAATCTCGGC | CTGGCAAACC | GGGGCGTCGT | GAACATTCTC | 1260 |
| GGCAACGCCA | ACATCGGCAA | TTACAACATT | CTCGGCAGCG | GAAACGTCGG | TGACTTCAAC | 1320 |
| ATCCTTGGCA | GCGGCAACCT | CGGCAGCCAA | AACATCTTGG | GCAGCGGCAA | CGTCGGCAGC | 1380 |
| TTCAATATCG | GCAGTGGAAG | CATCGGAGTA | TTCAATGTCT | GTTCCGGAAG | CCTGGGAAAC | 1440 |
| TACAACATCG | GATCCGGAAA | CCTCGGGATC | TACAACATCG | GTTTTGGAAA | CGTCGGCGAC | 1500 |
| TACAACGTCG | GCTTCGGGAA | CGCGGGCGAC | TTCAACCAAG | GCTTTGCCAA | CACCGGCAAC | 1560 |
| AACAACATCG | GGTTCGCCAA | CACCGGCAAC | AACAACATCG | GCATCGGGCT | GTCCGGCGAC | 1620 |

AACCAGCAGG GCTTCAATAT TGCTAGCGGC TGGAACTCGG GCACCGGCAA CAGCGGCCTG 1680
 TTCAATTCGG GCACCAATAA CGTTGGCATC TTCAACGCGG GCACCGGAAA CGTCGGCATC 1740
 GCAAACTCGG GCACCGGGAA CTGGGGTATC GGAACCCGG GTACCGACAA TACCGGCATC 1800
 CTCAATGCTG GCAGCTACAA CACGGGCATC CTCAACGCCG GCGACTTCAA CACGGGCTTC 1860
 TACAACACGG GCAGCTACAA CACCGGCGGC TTCAACGTCG GTAACACCAA CACCGGCAAC 1920
 TTCAACGTGG GTGACACCAA TACCGGCAGC TATAACCCGG GTGACACCAA CACCGGCTTC 1980
 TTCAATCCCG GCAACGTCAA TACCGGCGCT TTCGACACGG GCGACTTCAA CAATGGCTTC 2040
 TTGGTGGCGG GCGATAACCA GGGCCAGATT GCCATCGATC TCTCGGTCAC CACTCCATTC 2100
 ATCCCCATAA ACGAGCAGAT GGTCATTGAC GTACACAACG TAATGACCTT CGGCGGCAAC 2160
 ATGATCACGG TCACCGAGGC CTCGACCGTT TTCCCCAAA CCTTCTATCT GAGCGGTTTG 2220
 TTCTTCTTCG GCCCGGTCAA TCTCAGCGCA TCCACGCTGA CCGTTCCGAC GATCACCTC 2280
 ACCATCGGCG GACCGACGGT GACCGTCCCC ATCAGCATTG TCGGTGCTCT GGAGAGCCGC 2340
 ACGATTACCT TCCTCAAGAT CGATCCGGCG CCGGGCATCG GAAATTCGAC CACCAACCCC 2400
 TCGTCCGGCT TCTTCAACTC GGGCACCGGT GGCACATCTG GCTTCCAAA CGTCGGCGGC 2460
 GGCAGTTCAG GCGTCTGGAA CAGTGGTTTG AGCAGCGCGA TAGGGAATTC GGGTTTCCAG 2520
 AACCTCGGCT CGCTGCAGTC AGGCTGGGCG AACCTGGGCA ACTCCGTATC GGGCTTTTTT 2580
 AACACCAGTA CGGTGAACCT CTCCACGCCG GCCAATGTCT CGGGCCTGAA CAACATCGGC 2640
 ACCAACCTGT CCGGCGTGTT CCGCGGTCCG ACCGGGACGA TTTTCAACGC GGGCCTTGCC 2700
 AACCTGGGCC AGTTGAACAT CGGCAGCGCC TCGTGCCGAA TTCGGCACGA GTTAGATACG 2760
 GTTTCAACAA TCATATCCGC GTTTTGCGGC AGTGATCAG ACGAATCGAA CCCGGGAAGC 2820
 GTAAGCGAAT AAACCGAATG GCGGCCTGTC AT 2852

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Gly Gln Asn Ala Pro Ala Ile Ala Ala Thr Glu Ala Ala Tyr Asp Gln
 1 5 10 15

Met Trp Ala Gln Asp Val Ala Ala Met Phe Gly Tyr His Ala Gly Ala
 20 25 30
 Ser Ala Ala Val Ser Ala Leu Thr Pro Phe Gly Gln Ala Leu Pro Thr
 35 40 45
 Val Ala Gly Gly Gly Ala Leu Val Ser Ala Ala Ala Ala Gln Val Thr
 50 55 60
 Thr Arg Val Phe Arg Asn Leu Gly Leu Ala Asn Val Arg Glu Gly Asn
 65 70 75 80
 Val Arg Asn Gly Asn Val Arg Asn Phe Asn Leu Gly Ser Ala Asn Ile
 85 90 95
 Gly Asn Gly Asn Ile Gly Ser Gly Asn Ile Gly Ser Ser Asn Ile Gly
 100 105 110
 Phe Gly Asn Val Gly Pro Gly Leu Thr Ala Ala Leu Asn Asn Ile Gly
 115 120 125
 Phe Gly Asn Thr Gly Ser Asn Asn Ile Gly Phe Gly Asn Thr Gly Ser
 130 135 140
 Asn Asn Ile Gly Phe Gly Asn Thr Gly Asp Gly Asn Arg Gly Ile Gly
 145 150 155 160
 Leu Thr Gly Ser Gly Leu Leu Gly Phe Gly Gly Leu Asn Ser Gly Thr
 165 170 175
 Gly Asn Ile Gly Leu Phe Asn Ser Gly Thr Gly Asn Val Gly Ile Gly
 180 185 190
 Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn Ser Gly Asn Ser Tyr
 195 200 205
 Asn Thr Gly Phe Gly Asn Ser Gly Asp Ala Asn Thr Gly Phe Phe Asn
 210 215 220
 Ser Gly Ile Ala Asn Thr Gly Val Gly Asn Ala Gly Asn Tyr Asn Thr
 225 230 235 240
 Gly Ser Tyr Asn Pro Gly Asn Ser Asn Thr Gly Gly Phe Asn Met Gly
 245 250 255
 Gln Tyr Asn Thr Gly Tyr Leu Asn Ser Gly Asn Tyr Asn Thr Gly Leu
 260 265 270
 Ala Asn Ser Gly Asn Val Asn Thr Gly Ala Phe Ile Thr Gly Asn Phe
 275 280 285
 Asn Asn Gly Phe Leu Trp Arg Gly Asp His Gln Gly Leu Ile Phe Gly
 290 295 300
 Ser Pro Gly Phe Phe Asn Ser Thr Ser Ala Pro Ser Ser Gly Phe Phe

10084843 022502
 2002220 E484800T

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| 305 | | | | | 310 | | | | 315 | | | | 320 | | | |
| Asn | Ser | Gly | Ala | Gly | Ser | Ala | Ser | Gly | Phe | Leu | Asn | Ser | Gly | Ala | Asn | |
| | | | | 325 | | | | 330 | | | | 335 | | | | |
| Asn | Ser | Gly | Phe | Phe | Asn | Ser | Ser | Ser | Gly | Ala | Ile | Gly | Asn | Ser | Gly | |
| | | | | 340 | | | | 345 | | | | 350 | | | | |
| Leu | Ala | Asn | Ala | Gly | Val | Leu | Val | Ser | Gly | Val | Ile | Asn | Ser | Gly | Asn | |
| | | | | 355 | | | | 360 | | | | 365 | | | | |
| Thr | Val | Ser | Gly | Leu | Phe | Asn | Met | Ser | Leu | Val | Ala | Ile | Thr | Thr | Pro | |
| | | | | 370 | | | | 375 | | | | 380 | | | | |
| Ala | Leu | Ile | Ser | Gly | Phe | Phe | Asn | Thr | Gly | Ser | Asn | Met | Ser | Gly | Phe | |
| 385 | | | | 390 | | | | 395 | | | | 400 | | | | |
| Phe | Gly | Gly | Pro | Pro | Val | Phe | Asn | Leu | Gly | Leu | Ala | Asn | Arg | Gly | Val | |
| | | | | 405 | | | | 410 | | | | 415 | | | | |
| Val | Asn | Ile | Leu | Gly | Asn | Ala | Asn | Ile | Gly | Asn | Tyr | Asn | Ile | Leu | Gly | |
| | | | | 420 | | | | 425 | | | | 430 | | | | |
| Ser | Gly | Asn | Val | Gly | Asp | Phe | Asn | Ile | Leu | Gly | Ser | Gly | Asn | Leu | Gly | |
| | | | | 435 | | | | 440 | | | | 445 | | | | |
| Ser | Gln | Asn | Ile | Leu | Gly | Ser | Gly | Asn | Val | Gly | Ser | Phe | Asn | Ile | Gly | |
| | | | | 450 | | | | 455 | | | | 460 | | | | |
| Ser | Gly | Asn | Ile | Gly | Val | Phe | Asn | Val | Gly | Ser | Gly | Ser | Leu | Gly | Asn | |
| 465 | | | | 470 | | | | 475 | | | | 480 | | | | |
| Tyr | Asn | Ile | Gly | Ser | Gly | Asn | Leu | Gly | Ile | Tyr | Asn | Ile | Gly | Phe | Gly | |
| | | | | 485 | | | | 490 | | | | 495 | | | | |
| Asn | Val | Gly | Asp | Tyr | Asn | Val | Gly | Phe | Gly | Asn | Ala | Gly | Asp | Phe | Asn | |
| | | | | 500 | | | | 505 | | | | 510 | | | | |
| Gln | Gly | Phe | Ala | Asn | Thr | Gly | Asn | Asn | Asn | Ile | Gly | Phe | Ala | Asn | Thr | |
| | | | | 515 | | | | 520 | | | | 525 | | | | |
| Gly | Asn | Asn | Asn | Ile | Gly | Ile | Gly | Leu | Ser | Gly | Asp | Asn | Gln | Gln | Gly | |
| | | | | 530 | | | | 535 | | | | 540 | | | | |
| Phe | Asn | Ile | Ala | Ser | Gly | Trp | Asn | Ser | Gly | Thr | Gly | Asn | Ser | Gly | Leu | |
| 545 | | | | 550 | | | | 555 | | | | 560 | | | | |
| Phe | Asn | Ser | Gly | Thr | Asn | Asn | Val | Gly | Ile | Phe | Asn | Ala | Gly | Thr | Gly | |
| | | | | 565 | | | | 570 | | | | 575 | | | | |
| Asn | Val | Gly | Ile | Ala | Asn | Ser | Gly | Thr | Gly | Asn | Trp | Gly | Ile | Gly | Asn | |
| | | | | 580 | | | | 585 | | | | 590 | | | | |
| Pro | Gly | Thr | Asp | Asn | Thr | Gly | Ile | Leu | Asn | Ala | Gly | Ser | Tyr | Asn | Thr | |
| | | | | 595 | | | | 600 | | | | 605 | | | | |

Gly Ile Leu Asn Ala Gly Asp Phe Asn Thr Gly Phe Tyr Asn Thr Gly
 610 615 620
 Ser Tyr Asn Thr Gly Gly Phe Asn Val Gly Asn Thr Asn Thr Gly Asn
 625 630 635 640
 Phe Asn Val Gly Asp Thr Asn Thr Gly Ser Tyr Asn Pro Gly Asp Thr
 645 650 655
 Asn Thr Gly Phe Phe Asn Pro Gly Asn Val Asn Thr Gly Ala Phe Asp
 660 665 670
 Thr Gly Asp Phe Asn Asn Gly Phe Leu Val Ala Gly Asp Asn Gln Gly
 675 680 685
 Gln Ile Ala Ile Asp Leu Ser Val Thr Thr Pro Phe Ile Pro Ile Asn
 690 695 700
 Glu Gln Met Val Ile Asp Val His Asn Val Met Thr Phe Gly Gly Asn
 705 710 715 720
 Met Ile Thr Val Thr Glu Ala Ser Thr Val Phe Pro Gln Thr Phe Tyr
 725 730 735
 Leu Ser Gly Leu Phe Phe Phe Gly Pro Val Asn Leu Ser Ala Ser Thr
 740 745 750
 Leu Thr Val Pro Thr Ile Thr Leu Thr Ile Gly Gly Pro Thr Val Thr
 755 760 765
 Val Pro Ile Ser Ile Val Gly Ala Leu Glu Ser Arg Thr Ile Thr Phe
 770 775 780
 Leu Lys Ile Asp Pro Ala Pro Gly Ile Gly Asn Ser Thr Thr Asn Pro
 785 790 795 800
 Ser Ser Gly Phe Phe Asn Ser Gly Thr Gly Gly Thr Ser Gly Phe Gln
 805 810 815
 Asn Val Gly Gly Gly Ser Ser Gly Val Trp Asn Ser Gly Leu Ser Ser
 820 825 830
 Ala Ile Gly Asn Ser Gly Phe Gln Asn Leu Gly Ser Leu Gln Ser Gly
 835 840 845
 Trp Ala Asn Leu Gly Asn Ser Val Ser Gly Phe Phe Asn Thr Ser Thr
 850 855 860
 Val Asn Leu Ser Thr Pro Ala Asn Val Ser Gly Leu Asn Asn Ile Gly
 865 870 875 880
 Thr Asn Leu Ser Gly Val Phe Arg Gly Pro Thr Gly Thr Ile Phe Asn
 885 890 895

205220" E434800T

Ala Gly Leu Ala Asn Leu Gly Gln Leu Asn Ile Gly Ser Ala Ser Cys
 900 905 910

Arg Ile Arg His Glu Leu Asp Thr Val Ser Thr Ile Ile Ser Ala Phe
 915 920 925

Cys Gly Ser Ala Ser Asp Glu Ser Asn Pro Gly Ser Val Ser Glu
 930 935 940

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGATCGA CATCATCGGG ACC 53

(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

CCTGAATTCA GGCCTCGGTT GCGCCGGCCT CATCTTGAAC GA 42

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GGATCCTGCA GGCTCGAAAC CACCGAGCGG T 31

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

205220" E4848001

CTCTGAATTC AGCGCTGGAA ATCGTCGCGA T

31

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGATCCAGCG CTGAGATGAA GACCGATGCC GCT

33

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GGATATCTGC AGAATTCAGG TTAAAGCCC ATTTGCGA

38

(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CCGCATGCGA GCCACGTGCC CACAACGGCC

30

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

CTTCATGGAA TTCTCAGGCC GGTAAGGTCC GCTGCGG

37

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7676 base pairs
 - (B) TYPE: nucleic acid

20040404 04040404

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

| | |
|--|------|
| TGGCGAATGG GACGCGCCCT GTAGCGGCGC ATTAAGCGCG GCGGGTGTGG TGGTTACGCG | 60 |
| CAGCGTGACC GCTACACTTG CCAGCGCCCT AGCGCCCGCT CCTTTCGCTT TCTTCCCTTC | 120 |
| CTTTCTCGCC ACGTTCGCCG GCTTTCCTCCG TCAAGCTCTA AATCGGGGGC TCCCTTTAGG | 180 |
| GTTCCGATTT AGTGCTTTAC GGCACCTCGA CCCCCAAAAA CTTGATTAGG GTGATGGTTC | 240 |
| ACGTAGTGGG CCATCGCCCT GATAGACGGT TTTTCGCCCT TTGACGTTGG AGTCCACGTT | 300 |
| CTTTAATAGT GGACTCTTGT TCCAAACTGG AACAACTC AACCCCTATCT CGGTCTATTC | 360 |
| TTTTGATTTA TAAGGGATTT TGCCGATTTT GGCCTATTGG TTAAAAAATG AGCTGATTTA | 420 |
| ACAAAAATTT AACGCGAATT TTAACAAAT ATTAACGTTT ACAATTCAG GTGGCACTTT | 480 |
| TCGGGGAAAT GTGCGCGGAA CCCCTATTTG TTTATTTTTC TAAATACATT CAAATATGTA | 540 |
| TCCGCTCATG AATTAATTCT TAGAAAACT CATCGAGCAT CAAATGAAAC TGCAATTTAT | 600 |
| TCATATCAGG ATTATCAATA CCATATTTTT GAAAAGCCG TTTCTGTAAT GAAGGAGAAA | 660 |
| ACTCACCGAG GCAGTTCCAT AGGATGGCAA GATCCTGGTA TCGGTCTGCG ATTCCGACTC | 720 |
| GTCCAACATC AATACAACCT ATTAATTTCC CCTCGTCAAA AATAAGGTTA TCAAGTGAGA | 780 |
| AATCACCATG AGTGACGACT GAATCCGGTG AGAATGGCAA AAGTTTATGC ATTTCTTTCC | 840 |
| AGACTTGTTT AACAGGCCAG CCATTACGCT CGTCATCAAA ATCACTCGCA TCAACCAAAC | 900 |
| CGTTATTCAT TCGTGATTGC GCCTGAGCGA GACGAAATAC GCGATCGCTG TTAAAAGGAC | 960 |
| AATTACAAAC AGGAATCGAA TGCAACCGGC GCAGGAACAC TGCCAGCGCA TCAACAATAT | 1020 |
| TTTCACCTGA ATCAGGATAT TCTTCTAATA CCTGGAATGC TGTTTTCCCG GGGATCGCAG | 1080 |
| TGGTGAGTAA CCATGCATCA TCAGGAGTAC GGATAAAATG CTTGATGGTC GGAAGAGGCA | 1140 |
| TAAATTCCGT CAGCCAGTTT AGTCTGACCA TCTCATCTGT AACATCATTG GCAACGCTAC | 1200 |
| CTTTGCCATG TTTCAGAAAC AACTCTGGCG CATCGGGCTT CCCATACAAT CGATAGATTG | 1260 |
| TCGCACCTGA TTGCCCAGCA TTATCGCGAG CCCATTTATA CCCATATAAA TCAGCATCCA | 1320 |
| TGTTGGAATT TAATCGCGGC CTAGAGCAAG ACGTTTCCCG TTGAATATGG CTCATAACAC | 1380 |
| CCCTTGATT ACTGTTTATG TAAGCAGACA GTTTTATTGT TCATGACCAA AATCCCTTAA | 1440 |
| CGTGAGTTTT CGTTCCACTG AGCGTCAGAC CCCGTAGAAA AGATCAAAGG ATCTTCTTGA | 1500 |

GATCCTTTTT TTCTGCGCGT AATCTGCTGC TTGCAAACAA AAAAACCACC GCTACCAGCG 1560
 GTGGTTTGTT TGCCGGATCA AGAGCTACCA ACTCTTTTTC CGAAGGTAAC TGGCTTCAGC 1620
 AGAGCGCAGA TACCAAATAC TGTCCTTCTA GTGTAGCCGT AGTTAGGCCA CCACTTCAAG 1680
 AACTCTGTAG CACCGCCTAC ATACCTCGCT CTGCTAATCC TGTACCAGT GGCTGCTGCC 1740
 AGTGGCGATA AGTCGTGTCT TACCGGGTTG GACTCAAGAC GATAGTTACC GGATAAGGCG 1800
 CAGCGGTCGG GCTGAACGGG GGGTTCGTGC ACACAGCCCA GCTTGGAGCG AACGACCTAC 1860
 ACCGAACTGA GATACCTACA GCGTGAGCTA TGAGAAAGCG CCACGCTTCC CGAAGGGAGA 1920
 AAGGCGGACA GGTATCCGGT AAGCGGCAGG GTCGGAACAG GAGAGCGCAC GAGGGAGCTT 1980
 CCAGGGGGAA ACGCCTGGTA TCTTTATAGT CCTGTGCGGT TTCGCCACCT CTGACTTGAG 2040
 CGTCGATTTT TGTGATGCTC GTCAGGGGGG CGGAGCCTAT GGAAAAACGC CAGCAACGCG 2100
 GCCTTTTAC GGTTCCTGGC CTTTTGCTGG CCTTTTGCTC ACATGTTCTT TCCTGCGTTA 2160
 TCCCCTGATT CTGTGGATAA CCGTATTACC GCCTTTGAGT GAGCTGATAC CGCTCGCCGC 2220
 AGCCGAACGA CCGAGCGCAG CGAGTCAGTG AGCGAGGAAG CGGAAGAGCG CCTGATGCGG 2280
 TATTTTCTCC TTACGCATCT GTGCGGTATT TCACACCGCA TATATGGTGC ACTCTCAGTA 2340
 CAATCTGCTC TGATGCCGCA TAGTTAAGCC AGTATACACT CCGCTATCGC TACGTGACTG 2400
 GGTCATGGCT GCGCCCCGAC ACCCGCCAAC ACCCGCTGAC GCGCCCTGAC GGGCTTGTCT 2460
 GCTCCCGGCA TCCGCTTACA GACAAGCTGT GACCGTCTCC GGGAGCTGCA TGTGTCAGAG 2520
 GTTTTCACCG TCATCACC GAACGCGCGAG GCAGCTGCGG TAAAGCTCAT CAGCGTGGTC 2580
 GTGAAGCGAT TCACAGATGT CTGCCTGTTC ATCCGCGTCC AGCTCGTTGA GTTCTCCAG 2640
 AAGCGTTAAT GTCTGGCTTC TGATAAAGCG GGCCATGTTA AGGGCGGTTT TTTCTGTTT 2700
 GGTCACTGAT GCCTCCGTGT AAGGGGGATT TCTGTTTATG GGGGTAATGA TACCGATGAA 2760
 ACGAGAGAGG ATGCTCACGA TACGGGTTAC TGATGATGAA CATGCCCGGT TACTGGAACG 2820
 TTGTGAGGGT AAACAACTGG CGGTATGGAT GCGGCGGGAC CAGAGAAAAA TCACTCAGGG 2880
 TCAATGCCAG CGCTTCGTTA ATACAGATGT AGGTGTTCCA CAGGGTAGCC AGCAGCATCC 2940
 TGCGATGCAG ATCCGGAACA TAATGGTGCA GGGCGCTGAC TTCCGCGTTT CCAGACTTTA 3000
 CGAAACACGG AAACCGAAGA CCATTTCATGT TGTGCTCAG GTCGCAGACG TTTTGCAGCA 3060
 GCAGTCGCTT CACGTTGCTC CGCGTATCGG TGATTCATTC TGCTAACCAG TAAGGCAACC 3120
 CCGCCAGCCT AGCCGGGTCC TCAACGACAG GAGCACGATC ATGCGCACCC GTGGGGCCGC 3180

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| | | | | | | |
|------------|------------|------------|-------------|------------|------------|------|
| CATGCCGGCG | ATAATGGCCT | GCTTCTCGCC | GAAACGTTTG | GTGGCGGGAC | CAGTGACGAA | 3240 |
| GGCTTGAGCG | AGGGCGTGCA | AGATTCCGAA | TACCGCAAGC | GACAGGCCGA | TCATCGTCGC | 3300 |
| GCTCCAGCGA | AAGCGGTCCT | CGCCGAAAAT | GACCCAGAGC | GCTGCCGGGA | CCTGTCCTAC | 3360 |
| GAGTTGCATG | ATAAAGAAGA | CAGTCATAAG | TGCGGCGACG | ATAGTCATGC | CCCGCGCCCA | 3420 |
| CCGGAAGGAG | CTGACTGGGT | TGAAGGCTCT | CAAGGGCATC | GGTCGAGATC | CCGGTGCCTA | 3480 |
| ATGAGTGAGC | TAACCTACAT | TAATTGCGTT | GCGCTCACTG | CCCGCTTTCC | AGTCGGGAAA | 3540 |
| CCTGTGCTGC | CAGCTGCATT | AATGAATCGG | CCAACGCGCG | GGGAGAGGCG | GTTTGCGTAT | 3600 |
| TGGGCGCCAG | GGTGGTTTTT | CTTTTCACCA | GTGAGACGGG | CAACAGCTGA | TTGCCCTTCA | 3660 |
| CCGCCTGGCC | CTGAGAGAGT | TGCAGCAAGC | GGTCCACGCT | GGTTTGCCCC | AGCAGGCGAA | 3720 |
| AATCCTGTTT | GATGGTGGTT | AACGGCGGGA | TATAACATGA | GCTGTCTTCG | GTATCGTCGT | 3780 |
| ATCCCACTAC | CGAGATATCC | GCACCAACGC | GCAGCCCGGA | CTCGGTAATG | GCGCGCATTG | 3840 |
| CGCCCAGCGC | CATCTGATCG | TTGGCAACCA | GCATCGCAGT | GGGAACGATG | CCCTCATTCA | 3900 |
| GCATTTGCAT | GGTTTGTGTA | AAACCGGACA | TGGCACTCCA | GTGCGCTTCC | CGTTCCGCTA | 3960 |
| TCGGCTGAAT | TTGATTGCGA | GTGAGATATT | TATGCCAGCC | AGCCAGACGC | AGACGCGCCG | 4020 |
| AGACAGAACT | TAATGGGCCC | GCTAACAGCG | CGATTTGCTG | GTGACCCAAT | GCGACCAGAT | 4080 |
| GCTCCACGCC | CAGTCGCGTA | CCGTCTTCAT | GGGAGAAAAAT | AATACTGTTG | ATGGGTGTCT | 4140 |
| GGTCAGAGAC | ATCAAGAAAT | AACGCCGGAA | CATTAGTGCA | GGCAGCTTCC | ACAGCAATGG | 4200 |
| CATCCTGGTC | ATCCAGCGGA | TAGTTAATGA | TCAGCCCACT | GACGCGTTGC | GCGAGAAGAT | 4260 |
| TGTGCACCGC | CGCTTTACAG | GCTTCGACGC | CGCTTCGTTT | TACCATCGAC | ACCACCACGC | 4320 |
| TGGCACCCAG | TTGATCGGCG | CGAGATTTAA | TCGCCGCGAC | AATTTGCGAC | GGCGCGTGCA | 4380 |
| GGGCCAGACT | GGAGGTGGCA | ACGCCAATCA | GCAACGACTG | TTTGCCCGCC | AGTTGTTGTG | 4440 |
| CCACGCGGTT | GGGAATGTAA | TTGAGCTCCG | CCATCGCCGC | TTCCACTTTT | TCCGCGTTTT | 4500 |
| TCGAGAAAC | GTGGCTGGCC | TGGTTCACCA | CGCGGGAAAC | GGTCTGATAA | GAGACACCGG | 4560 |
| CATACTCTGC | GACATCGTAT | AACGTTACTG | GTTTCACATT | CACCACCCTG | AATTGACTCT | 4620 |
| CTTCCGGGCG | CTATCATGCC | ATACCGCGAA | AGGTTTTGCG | CCATTCGATG | GTGTCCGGGA | 4680 |
| TCTCGACGCT | CTCCCTTATG | CGACTCCTGC | ATTAGGAAGC | AGCCCAGTAG | TAGGTTGAGG | 4740 |
| CCGTTGAGCA | CCGCCGCCGC | AAGGAATGGT | GCATGCAAGG | AGATGGCGCC | CAACAGTCCC | 4800 |

CCGGCCACGG GGCCTGCCAC CATACCACG CCGAAACAAG CGCTCATGAG CCCGAAGTGG 4860
 CGAGCCCGAT CTTCCCATC GGTGATGTCG GCGATATAGG CGCCAGCAAC CGCACCTGTG 4920
 GCGCCGGTGA TGCCGGCCAC GATGCGTCCG GCGTAGAGGA TCGAGATCTC GATCCCGCGA 4980
 AATTAATACG ACTCACTATA GGGGAATTGT GAGCGGATAA CAATTCCCCT CTAGAAATAA 5040
 TTTTGTTTAA CTTTAAGAAG GAGATATACA TATGGGCCAT CATCATCATC ATCACGTGAT 5100
 CGACATCATC GGGACCAGCC CCACATCCTG GGAACAGGCG GCGGCGGAGG CGGTCCAGCG 5160
 GGCGCGGGAT AGCGTCGATG ACATCCGCGT CGCTCGGGTC ATTGAGCAGG ACATGGCCGT 5220
 GGACAGCGCC GGCAAGATCA CCTACCGCAT CAAGCTCGAA GTGTCGTTCA AGATGAGGCC 5280
 GGCGCAACCG AGGGGCTCGA AACCACCGAG CGGTTGCGCT GAAACGGGCG CCGGCGCCGG 5340
 TACTGTCGCG ACTACCCCG CGTCGTCGCC GGTGACGTTG GCGGAGACCG GTAGCACGCT 5400
 GCTCTACCCG CTGTTCAACC TGTGGGTCC GGCCTTTCAC GAGAGGTATC CGAACGTCAC 5460
 GATCACCGCT CAGGGCACCG GTTCTGGTGC CGGGATCGCG CAGGCCGCCG CCGGGACGGT 5520
 CAACATTGGG GCCTCCGACG CCTATCTGTC GGAAGGTGAT ATGGCCGCGC ACAAGGGGCT 5580
 GATGAACATC GCGCTAGCCA TCTCCGCTCA GCAGGTCAAC TACAACCTGC CCGGAGTGAG 5640
 CGAGCACCTC AAGCTGAACG GAAAAGTCCT GGCGGCCATG TACCAGGGCA CCATCAAAAC 5700
 CTGGGACGAC CCGCAGATCG CTGCGCTCAA CCCCGGCGTG AACCTGCCCC GCACCGCGGT 5760
 AGTTCCGCTG CACCGCTCCG ACGGGTCCGG TGACACCTTC TTGTTACCC AGTACCTGTC 5820
 CAAGCAAGAT CCCGAGGGCT GGGGCAAGTC GCCCGGCTTC GGCACCACCG TCGACTTCCC 5880
 GGCGGTGCCG GGTGCGCTGG GTGAGAACGG CAACGGCGGC ATGGTGACCG GTTGCGCCGA 5940
 GACACCGGGC TCGTGGCCT ATATCGGCAT CAGCTTCCTC GACCAGGCCA GTCAACGGGG 6000
 ACTCGGCGAG GCCCAACTAG GCAATAGCTC TGGCAATTTT TTGTTGCCCC ACGCGCAAAG 6060
 CATTAGGCC GCGGCGGCTG GCTTCGCATC GAAAACCCCG GCGAACCAGG CGATTTTCAT 6120
 GATCGACGGG CCCGCCCCGG ACGGCTACCC GATCATCAAC TACGAGTACG CCATCGTCAA 6180
 CAACGGGCAA AAGGACGCCG CCACGCGCA GACCTTGACG GCATTTCTGC ACTGGGCGAT 6240
 CACCGACGGC AACAAGGCCT CGTTCCTCGA CCAGGTTTCAT TTCCAGCCGC TGCCGCCCCG 6300
 GGTGGTGAAG TTGTCTGACG CGTTGATCGC GACGATTTCC AGCGCTGAGA TGAAGACCGA 6360
 TGCCGCTACC CTCGCGCAGG AGGCAGGTAA TTTCGAGCGG ATCTCCGCGC ACCTGAAAAC 6420
 CCAGATCGAC CAGGTGGAGT CGACGGCAGG TTCGTTGCAG GGCCAGTGGC GCGGCGCGGC 6480

(2) INFORMATION FOR SEQ ID NO:214:

(A) LENGTH: 802 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

Met Gly His His His His His His Val Ile Asp Ile Ile Gly Thr Ser
1 5 10 15

Pro Thr Ser Trp Glu Gln Ala Ala Ala Glu Ala Val Gln Arg Ala Arg

| 20 | | | | | 25 | | | | | 30 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ser | Val | Asp | Asp | Ile | Arg | Val | Ala | Arg | Val | Ile | Glu | Gln | Asp | Met |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Ala | Val | Asp | Ser | Ala | Gly | Lys | Ile | Thr | Tyr | Arg | Ile | Lys | Leu | Glu | Val |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ser | Phe | Lys | Met | Arg | Pro | Ala | Gln | Pro | Arg | Gly | Ser | Lys | Pro | Pro | Ser |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Gly | Ser | Pro | Glu | Thr | Gly | Ala | Gly | Ala | Gly | Thr | Val | Ala | Thr | Thr | Pro |
| | | | | 85 | | | | | | 90 | | | | 95 | |
| Ala | Ser | Ser | Pro | Val | Thr | Leu | Ala | Glu | Thr | Gly | Ser | Thr | Leu | Leu | Tyr |
| | | | 100 | | | | | | | 105 | | | 110 | | |
| Pro | Leu | Phe | Asn | Leu | Trp | Gly | Pro | Ala | Phe | His | Glu | Arg | Tyr | Pro | Asn |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Val | Thr | Ile | Thr | Ala | Gln | Gly | Thr | Gly | Ser | Gly | Ala | Gly | Ile | Ala | Gln |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Ala | Ala | Ala | Gly | Thr | Val | Asn | Ile | Gly | Ala | Ser | Asp | Ala | Tyr | Leu | Ser |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Glu | Gly | Asp | Met | Ala | Ala | His | Lys | Gly | Leu | Met | Asn | Ile | Ala | Leu | Ala |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Ile | Ser | Ala | Gln | Gln | Val | Asn | Tyr | Asn | Leu | Pro | Gly | Val | Ser | Glu | His |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Leu | Lys | Leu | Asn | Gly | Lys | Val | Leu | Ala | Ala | Met | Tyr | Gln | Gly | Thr | Ile |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Lys | Thr | Trp | Asp | Asp | Pro | Gln | Ile | Ala | Ala | Leu | Asn | Pro | Gly | Val | Asn |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Leu | Pro | Gly | Thr | Ala | Val | Val | Pro | Leu | His | Arg | Ser | Asp | Gly | Ser | Gly |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Asp | Thr | Phe | Leu | Phe | Thr | Gln | Tyr | Leu | Ser | Lys | Gln | Asp | Pro | Glu | Gly |
| | | | 245 | | | | | | 250 | | | | | 255 | |
| Trp | Gly | Lys | Ser | Pro | Gly | Phe | Gly | Thr | Thr | Val | Asp | Phe | Pro | Ala | Val |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Pro | Gly | Ala | Leu | Gly | Glu | Asn | Gly | Asn | Gly | Gly | Met | Val | Thr | Gly | Cys |
| | 275 | | | | | | 280 | | | | | 285 | | | |
| Ala | Glu | Thr | Pro | Gly | Cys | Val | Ala | Tyr | Ile | Gly | Ile | Ser | Phe | Leu | Asp |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Gln | Ala | Ser | Gln | Arg | Gly | Leu | Gly | Glu | Ala | Gln | Leu | Gly | Asn | Ser | Ser |
| 305 | | | | | 310 | | | | | 315 | | | | 320 | |

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Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala
 325 330 335
 Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp
 340 345 350
 Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile
 355 360 365
 Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala
 370 375 380
 Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp
 385 390 395 400
 Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp
 405 410 415
 Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala
 420 425 430
 Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu
 435 440 445
 Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly
 450 455 460
 Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg
 465 470 475 480
 Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser
 485 490 495
 Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu
 500 505 510
 Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala
 515 520 525
 Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro
 530 535 540
 Val Ala Pro Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro
 545 550 555 560
 Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro
 565 570 575
 Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn
 580 585 590
 Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser
 595 600 605

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Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr
 610 615 620
 Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr
 625 630 635 640
 Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu
 645 650 655
 Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu
 660 665 670
 Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser
 675 680 685
 Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys
 690 695 700
 Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile
 705 710 715 720
 Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp
 725 730 735
 Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala
 740 745 750
 Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro
 755 760 765
 Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala
 770 775 780
 Gly Glu Val Ala Pro Thr Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu
 785 790 795 800
 Pro Ala

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTGGCGGCGC | TGCGGCCGGC | CAGCAGAGCG | ATGTGCATCC | GTTCGCGAAC | CTGATCGCGG | 60 |
| TCGACGATGA | GCGCGCCGAA | CGCCGCGACG | ACGAAGAACG | TCAGGAAGCC | GTCCAGCAGC | 120 |
| GCGGTCCGCG | CGGTGACGAA | GCTGACCCCG | TCGCAGATCA | GCAGCACCCC | GGCGATGGCG | 180 |
| CCGACCAATG | TCGACCGGCT | GATCCGCCCG | ACGATCCGCA | CCACCAGCGC | CACCAGGACC | 240 |
| ACACCCAGCA | GGGCGCCGGT | GAACCGCCAG | CCGAATCCGT | TGTGACCGAA | GATGGCCTCC | 300 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCGATCGCGA | TCAGCTGCTT | ACCGACCGGC | GGGTGAACCA | CCAGGCCGTA | CCCGGGGTTG | 360 |
| TCTTCCACCC | CATGGTTGTT | CAGCACCTGC | CAGGCCTGGC | GGTGCGTAAT | GCTTCTCGTC | 420 |
| GAAGATGGGG | GTGCCGGCAT | CCGTCACCGA | GCCC | | | 454 |

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TGCAGAAGTA | CGGCGGATCC | TCGGTGCCG | ACGCCGAACG | GATTCGCCGC | GTCGCCGAAC | 60 |
| GCATCGTCGC | CACCAAGAAG | CAAGGCAATG | ACGTCGTCGT | CGTCGTCTCT | GCCATGGGGG | 120 |
| ATACCACCGA | CGACCTGCTG | GATCTGGCTC | AGCAGGTGTG | CCCGGCGCCG | CCGCCTCGGG | 180 |
| AGCTGGACAT | GCTGCTTACC | GCCGGTGAAC | GCATCTCGAA | TGCGTTGGTG | GCCATGGCCA | 240 |
| TCGAGTCGCT | CGGCGCGCAT | GCCCCGTCGT | TCACCGGTTT | GCAGGCCGGG | GTGATCACCA | 300 |
| CCGGCACCCA | CGGCAACGCC | AAGATCATCG | ACGTCACGCC | GGGGCGGCTG | CAAACCGCCC | 360 |
| TTGAGGAAGG | GCGGGTCGTC | TTGGTGCCG | GATTCCAAGG | GGTCAGCCAG | GACACCAAGG | 420 |
| ATGTCACGAC | GTTGGGCCGC | GCGGCTCGG | ACACCACCGC | CGTCGCCATG | | 470 |

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GGCCGGCGTA | CCCGGCCGGG | ACAAACAACG | ATCGATTGAT | ATCGATGAGA | GACGGAGGAA | 60 |
| TCGTGGCCCT | TCCCCAGTTG | ACCGACGAGC | AGCGCGCGGC | CGCGTTGGAG | AAGGCTGCTG | 120 |
| CCGCACGTCG | AGCGCGAGCA | GAGCTCAAGG | ATCGGCTCAA | GCGTGGCGGC | ACCAACCTCA | 180 |
| CCCAGGTCCT | CAAGGACGCG | GAGAGCGATG | AAGTCTTGCG | CAAAATGAAG | GTGTCTGCGC | 240 |
| TGCTTGAGGC | CTTGCCAAAG | GTGGGCAAGG | TCCAGGCGC | | | 279 |

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACACGGTCGA | ACTCGACGAG | CCCCTCGTGG | AGGTGTCGAC | CGACAAGGTC | GACACCGAAA | 60 |
| TCCCTCGCCG | GCCGCGGGTG | TGCTGACCAA | GATCATCGCC | CAAGAAGATG | ACACGGTCGA | 120 |
| GGTCGGCGGC | GAGCTCTCTG | TCATTGGCGA | CGCCCATGAT | GCCGGCGAGG | CCGCGGTCCC | 180 |
| GGCACCCAG | AAAGTCTCTG | CCGGCCCAAC | CCGAATCCA | | | 219 |

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TCGCTGCCGA | CATCGGCGCC | GCGCCCGCCC | CCAAGCCCGC | ACCCAAGCCC | GTCCCCGAGC | 60 |
| CAGCGCCGAC | GCCGAAGGCC | GAACCCGCAC | CATCGCCGCC | GGCGGCCCAG | CCAGCCGGTG | 120 |
| CGGCCGAGGG | CGCACCGTAC | GTGACGCCGC | TGGTGCGAAA | GCTGGCGTCG | GAAAACAACA | 180 |
| TCGACCTCGC | CGGGGTGACC | GGCACCGGAG | TGGGTGGTCG | CATCCGCAAA | CAGGATGTGC | 240 |
| TGGCCGCGGC | TGAACAAAAG | AAGCGGGCGA | AAGCACCGGC | GCCGGCCGCC | CAGGCCGCCG | 300 |
| CCGCGCCGGC | CCCGAAAGCG | CCGCCTGAAG | ATCCGATGCC | GC | | 342 |

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GGGTCTTGGT | CAGTATCAGC | GCCGACGAGG | ACGCCACGGT | GCCCGTCGGC | GGCGAGTTGG | 60 |
| CCCGGATCGG | TGTCGCTGCC | GACATCGGCG | CCGCGCCCGC | CCCCAAGCCC | GCACCCAAGC | 120 |
| CCGTCCCCGA | GCCAGCGCCG | ACGCCGAAGG | CCGAACCCGC | ACCATCGCCG | CCGGCGGCCC | 180 |
| AGCCAGCCGG | TGCGGCCGAG | GGCGCACCGT | ACGTGACGCC | GCTGGTGCGA | AAGCTGGCGT | 240 |
| CGGAAAACAA | CATCGACCTC | GCCGGGGTGA | CCGGCACCGG | AGTGGGTGGT | CGCATCCGCA | 300 |
| AACAGGATGT | GCTGGCCGCG | GCTGAACAAA | AGAAGCGGGC | GAAAGCACCG | GCGCCCTGAG | 360 |
| CGCTTCATCA | CCCGGTTAAC | CAGCTTGCCC | CAGAAGCCGG | CTTCGACCTC | TTCGCGGGTC | 420 |
| TTGGTCCGCT | GCAGGCGGTC | GGCGAGCCAG | TTCAGGTTAG | GCGGCCGAAA | TCTTCCAGTT | 480 |
| CGCCAGGAAG | GGCACCCGGA | ACAGGGTCCG | CACCC | | | 515 |

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

| | | | | | | |
|-------------|------------|-------------|------------|------------|-------------|-----|
| CCGACCCCAA | GGTGCAGATT | CAACAGGCCA | TTGAGGAAGC | ACAGCGCACC | CACCAAGCGC | 60 |
| TGACTCAACA | GGCGGCGCAA | GTGATCGGTA | ACCAGCGTCA | ATTGGAGATG | CGACTCAACC | 120 |
| GACAGCTGGC | GGACATCGAA | AAGCTTCAGG | TCAATGTGCG | CCAAGCCCTG | ACGCTGGCCG | 180 |
| ACCAGGCCAC | CGCCGCCGGA | GACGCTGCCA | AGGCCACCGA | ATACAACAAC | GCCGCCGAGG | 240 |
| CGTTCGCAGC | CCAGCTGGTG | ACCGCCGAGC | AGAGCGTCGA | AGACCTCAAG | ACGCTGCATG | 300 |
| ACCAGGCGCT | TAGCGCCGCA | GCTCAGGCCA | AGAAGGCCGT | CGAACGAAAT | GCGATGGTGC | 360 |
| TGCAGCAGAA | GATCGCCGAG | CGAACCAAGC | TGCTCAGCCA | GCTCGAGCAG | GCGAAGATGC | 420 |
| AGGAGCAGGT | CAGCGCATCG | TTGCGGTCTGA | TGAGTGAGCT | CGCCGCGCCA | GGCAACACGC | 480 |
| CGAGCCTCGA | CGAGGTGCGC | GACAAGATCG | AGCGTCGCTA | CGCCAACGCG | ATCGGTTTCGG | 540 |
| CTGAACCTTGC | CGAGAGT | | | | | 557 |

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CAGGATAGGT | TTGACATCC | ACCTGGGTTT | CGCACCCGGT | GCGCGACCGT | GTGATAGGCC | 60 |
| AGAGGTGGAC | CTGCGCCGAC | CGACGATCGA | TCGAGGAGTC | AACAGAAATG | GCCTTCTCCG | 120 |
| TCCAGATGCC | GGCACTCGGT | GAGAGCGTCA | CCGAGGGGAC | GGTTACCCGC | TGGCTCAAAC | 180 |
| AGGAAGGCCA | CACGGTCGAA | CTCGACGAGC | CCCTCGTGGA | GGT | | 223 |

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| AAGAAGTACA | TCTGCCGGTC | GATGTCGGCG | AACCACGGCA | GCCAACCGGC | GCAGTAGCCG | 60 |
| ACCAGGACCA | CCGCATAACG | CCAGTCCCGG | CGCACAAACA | TACGCCACCC | CGCGTATGCC | 120 |
| AGGACTGGCA | CCGCCAGCCA | CCACATCGCG | GGCGTGCCGA | CCAGCATCTC | GGCCTTGACG | 180 |
| CACGACTGTG | CGCCGCAGCC | TGCAACGTCT | TGCTGGTCTGA | TGGCGTACAG | CACCGGCCGC | 240 |
| AACGACATGG | GCCAGGTCCA | CGGTTTGGAT | TCCCAAGGGT | GGTAGTTGCC | TGCGGAATTC | 300 |
| GTCAGGCCCG | CGTGGAAGTG | GAACGCTTTG | GCGGTGTATT | GCCAGAGCGA | GCGCACGGCG | 360 |
| TCGGGCAGCG | GAACAACCGA | GTTGCGACCG | ACCGCTTGAC | CGACCGCATG | CCGATCGATC | 420 |
| GCGGTCTCGG | ACGCGAACCA | CGGAGCGTAG | GTGGCCAGAT | AGACCGCGAA | CGGGATCAAC | 480 |
| CCCAGCGCAT | ACCCGCTGGG | AAGCACGTCA | CGCCGCACTG | TTCCCAGCCA | CGGTCTTTGC | 540 |
| ACTTGGTATG | AACGTCGCGC | CGCCACGTCA | ACGCCAGC | | | 578 |

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACAACGATCG | ATTGATATCG | ATGAGAGACG | GAGGAATCGT | GGCCCTTCCC | CAGTTGACCG | 60 |
| ACGAGCAGCG | CGCGGCCGCG | TTGGAGAAGG | CTGCTGCCGC | ACGTCGAGCG | CGAGCAGAGC | 120 |
| TCAAGGATCG | GCTCAAGCGT | GGCGGCACCA | ACCTCACCCA | GGTCCTCAAG | GACGCGGAGA | 180 |
| GCGATGAAGT | CTTGGGCAAA | ATGAAGGTGT | CTGCGTGTCT | TGAGGCCTTG | CCAAAGGTGG | 240 |
| GCAAGGTCAA | GGCGCAGGAG | ATCATGACCG | AGCTGGAAAT | TGCGCCCCAC | CCCGCCGCCT | 300 |
| TCGTGGCCTC | GGTGACCGTC | AGCGCAAGGC | CCTGTGGAA | AAGTTCGGCT | CCGCCTAACC | 360 |
| CCGCCGGCCG | ACGATGCGGG | CCGGAAGGCC | TGTGGTGGGC | GTACCCCGGC | ATACGGGGGA | 420 |
| GAAGCGGCCT | GACAGGGCCA | GCTCACAATT | CAGGCCGAAC | GCCCCGGTGG | GGGGGAACCC | 480 |
| CCCC | | | | | | 484 |

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AGGACTGGCA | CCGCCAGCCA | CCACATCGCG | GGCGTGCCGA | CCAGCATCTC | GGCCTTGACG | 60 |
| CACGACTGTG | CGCCGCAGCC | TGCAACGTCT | TGCTGGTCGA | TGGCGTACAG | CACCGGCCGC | 120 |
| AACGACATGG | GCCAGGTCCA | CGGTTTGGAT | TCCCAAGGGT | GGTAGTTGCC | TGCGGAATTC | 180 |
| GTCAGGCCCG | CGTGGAAGTG | GAACGCTTTG | GCGGTGTAGT | GCCAGAGCGA | GCGCACGGCG | 240 |
| TCGGGCAGCG | GAACAACCGA | GTTGCGACCG | ACCGCTTGAC | CGACCGCATG | CCGATCGATC | 300 |
| GCGGTCTCGG | ACGCGAACCA | CGGAGCGTAG | GTGGCCAGAT | AGACCGCGAA | CGGGATCAAC | 360 |
| CCCAGCGCAT | ACCCGCTGGG | AAGCACGTCA | CGCCGCACTG | TCCCCAGCCA | CGGTCTTTGC | 420 |
| ACTTGTAAT | GACGTCGCGC | CGCCACGTCT | AACGCCAGCG | CCATCGCGCC | GAAGAACAGC | 480 |
| ACGAAGTACA | CGCCGGACCA | CTTGGTGGCG | CAAGCCAATC | CCAAGCAGCA | CCCCGGC | 537 |

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

Gly Gly Ala Ala Ala Gly Gln Gln Ser Asp Val His Pro Phe Ala Asn
 1 5 10 15
 Leu Ile Ala Val Asp Asp Glu Arg Ala Glu Arg Arg Asp Asp Glu Glu
 20 25 30
 Arg Gln Glu Ala Val Gln Gln Arg Gly Pro Arg Gly Asp Glu Ala Asp
 35 40 45
 Pro Val Ala Asp Gln Gln His Pro Gly Asp Gly Ala Asp Gln Cys Arg
 50 55 60
 Pro Ala Asp Pro Pro His Asp Pro His His Gln Arg His Gln Asp His
 65 70 75 80
 Thr Gln Gln Gly Ala Gly Glu Pro Pro Ala Glu Ser Val Val Thr Glu
 85 90 95
 Asp Gly Leu Pro Asp Arg Asp Gln Leu Leu Thr Asp Arg Arg Val Asn
 100 105 110
 His Gln Ala Val Pro Gly Val Val Phe His Pro Met Val Val Gln His
 115 120 125
 Leu Pro Gly Leu Ala Val Arg
 130 135

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Gln Lys Tyr Gly Gly Ser Ser Val Ala Asp Ala Glu Arg Ile Arg Arg
 1 5 10 15
 Val Ala Glu Arg Ile Val Ala Thr Lys Lys Gln Gly Asn Asp Val Val
 20 25 30
 Val Val Val Ser Ala Met Gly Asp Thr Thr Asp Asp Leu Leu Asp Leu
 35 40 45
 Ala Gln Gln Val Cys Pro Ala Pro Pro Pro Arg Glu Leu Asp Met Leu
 50 55 60
 Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile
 65 70 75 80
 Glu Ser Leu Gly Ala His Ala Arg Ser Phe Thr Gly Ser Gln Ala Gly
 85 90 95
 Val Ile Thr Thr Gly Thr His Gly Asn Ala Lys Ile Ile Asp Val Thr
 100 105 110
 Pro Gly Arg Leu Gln Thr Ala Leu Glu Glu Gly Arg Val Val Leu Val
 115 120 125
 Ala Gly Phe Gln Gly Val Ser Gln Asp Thr Lys Asp Val Thr Thr Leu
 130 135 140
 Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala Met
 145 150 155

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

Pro Ala Tyr Pro Ala Gly Thr Asn Asn Asp Arg Leu Ile Ser Met Arg
 1          5          10          15
Asp Gly Gly Ile Val Ala Leu Pro Gln Leu Thr Asp Glu Gln Arg Ala
    20          25          30
Ala Ala Leu Glu Lys Ala Ala Ala Arg Arg Ala Arg Ala Glu Leu
    35          40          45
Lys Asp Arg Leu Lys Arg Gly Gly Thr Asn Leu Thr Gln Val Leu Lys
    50          55          60
Asp Ala Glu Ser Asp Glu Val Leu Gly Lys Met Lys Val Ser Ala Leu
    65          70          75          80
Leu Glu Ala Leu Pro Lys Val Gly Lys Val Gln Ala
          85          90

```

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```

Thr Val Glu Leu Asp Glu Pro Leu Val Glu Val Ser Thr Asp Lys Val
 1          5          10          15
Asp Thr Glu Ile Pro Ser Pro Ala Ala Gly Val Leu Thr Lys Ile Ile
    20          25          30
Ala Gln Glu Asp Asp Thr Val Glu Val Gly Gly Glu Leu Ser Val Ile
    35          40          45
Gly Asp Ala His Asp Ala Gly Glu Ala Ala Val Pro Ala Pro Gln Lys
    50          55          60
Val Ser Ala Gly Pro Thr Arg Ile
    65          70

```

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

205220" E44300T

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

```

Ala Ala Asp Ile Gly Ala Ala Pro Ala Pro Lys Pro Ala Pro Lys Pro
 1           5           10           15
Val Pro Glu Pro Ala Pro Thr Pro Lys Ala Glu Pro Ala Pro Ser Pro
          20           25           30
Pro Ala Ala Gln Pro Ala Gly Ala Ala Glu Gly Ala Pro Tyr Val Thr
          35           40           45
Pro Leu Val Arg Lys Leu Ala Ser Glu Asn Asn Ile Asp Leu Ala Gly
 50           55           60
Val Thr Gly Thr Gly Val Gly Gly Arg Ile Arg Lys Gln Asp Val Leu
65           70           75           80
Ala Ala Ala Glu Gln Lys Lys Arg Ala Lys Ala Pro Ala Pro Ala Ala
          85           90           95
Gln Ala Ala Ala Ala Pro Ala Pro Lys Ala Pro Pro Glu Asp Pro Met
          100          105          110
Pro

```

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

```

Val Leu Val Ser Ile Ser Ala Asp Glu Asp Ala Thr Val Pro Val Gly
 1           5           10           15
Gly Glu Leu Ala Arg Ile Gly Val Ala Ala Asp Ile Gly Ala Ala Pro
          20           25           30
Ala Pro Lys Pro Ala Pro Lys Pro Val Pro Glu Pro Ala Pro Thr Pro
          35           40           45
Lys Ala Glu Pro Ala Pro Ser Pro Pro Ala Ala Gln Pro Ala Gly Ala
 50           55           60
Ala Glu Gly Ala Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Ser
65           70           75           80
Glu Asn Asn Ile Asp Leu Ala Gly Val Thr Gly Thr Gly Val Gly Gly
          85           90           95
Arg Ile Arg Lys Gln Asp Val Leu Ala Ala Ala Glu Gln Lys Lys Arg
          100          105          110
Ala Lys Ala Pro Ala Pro
          115

```

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

205220 "E4843001"

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```

Asp Pro Lys Val Gln Ile Gln Gln Ala Ile Glu Glu Ala Gln Arg Thr
 1           5           10           15
His Gln Ala Leu Thr Gln Gln Ala Ala Gln Val Ile Gly Asn Gln Arg
          20           25           30
Gln Leu Glu Met Arg Leu Asn Arg Gln Leu Ala Asp Ile Glu Lys Leu
          35           40           45
Gln Val Asn Val Arg Gln Ala Leu Thr Leu Ala Asp Gln Ala Thr Ala
          50           55           60
Ala Gly Asp Ala Ala Lys Ala Thr Glu Tyr Asn Asn Ala Ala Glu Ala
65           70           75           80
Phe Ala Ala Gln Leu Val Thr Ala Glu Gln Ser Val Glu Asp Leu Lys
          85           90           95
Thr Leu His Asp Gln Ala Leu Ser Ala Ala Gln Ala Lys Lys Ala
          100          105          110
Val Glu Arg Asn Ala Met Val Leu Gln Gln Lys Ile Ala Glu Arg Thr
          115          120          125
Lys Leu Leu Ser Gln Leu Glu Gln Ala Lys Met Gln Glu Gln Val Ser
          130          135          140
Ala Ser Leu Arg Ser Met Ser Glu Leu Ala Ala Pro Gly Asn Thr Pro
145           150           155           160
Ser Leu Asp Glu Val Arg Asp Lys Ile Glu Arg Arg Tyr Ala Asn Ala
          165          170          175
Ile Gly Ser Ala Glu Leu Ala Glu Ser
          180          185

```

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```

Val Ser Thr Ser Thr Trp Val Pro His Pro Val Arg Asp Arg Val Ile
 1           5           10           15
Gly Gln Arg Trp Thr Cys Ala Asp Arg Arg Ser Ile Glu Glu Ser Thr
          20           25           30
Glu Met Ala Phe Ser Val Gln Met Pro Ala Leu Gly Glu Ser Val Thr
          35           40           45
Glu Gly Thr Val Thr Arg Trp Leu Lys Gln Glu Gly Asp Thr Val Glu
          50           55           60
Leu Asp Glu Pro Leu Val Glu
          65           70

```

(2) INFORMATION FOR SEQ ID NO:234:

205220-2488001

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

```

Glu Val His Leu Pro Val Asp Val Gly Glu Pro Arg Gln Pro Thr Gly
1      5      10      15
Ala Val Ala Asp Gln Asp His Arg Ile Thr Pro Val Pro Ala His Lys
      20      25      30
His Thr Pro Pro Arg Val Cys Gln Asp Trp His Arg Gln Pro Pro His
      35      40      45
Arg Gly Arg Ala Asp Gln His Leu Gly Leu Asp Ala Arg Leu Cys Ala
      50      55      60
Ala Ala Cys Asn Val Leu Leu Val Asp Gly Val Gln His Arg Pro Gln
      65      70      75      80
Arg His Gly Pro Gly Pro Arg Phe Gly Phe Pro Arg Val Val Val Ala
      85      90      95
Cys Gly Ile Arg Gln Ala Arg Val Glu Val Glu Arg Phe Gly Gly Val
      100     105     110
Leu Pro Glu Arg Ala His Gly Val Gly Gln Arg Asn Asn Arg Val Ala
      115     120     125
Thr Asp Arg Leu Thr Asp Arg Met Pro Ile Asp Arg Gly Leu Gly Arg
      130     135     140
Glu Pro Arg Ser Val Gly Gly Gln Ile Asp Arg Glu Arg Asp Gln Pro
      145     150     155     160
Gln Arg Ile Pro Ala Gly Lys His Val Thr Pro His Cys Ser Gln Pro
      165     170     175
Arg Ser Leu His Leu Val
      180

```

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

```

Asn Asp Arg Leu Ile Ser Met Arg Asp Gly Gly Ile Val Ala Leu Pro
1      5      10      15
Gln Leu Thr Asp Glu Gln Arg Ala Ala Ala Leu Glu Lys Ala Ala Ala
      20      25      30
Ala Arg Arg Ala Arg Ala Glu Leu Lys Asp Arg Leu Lys Arg Gly Gly
      35      40      45
Thr Asn Leu Thr Gln Val Leu Lys Asp Ala Glu Ser Asp Glu Val Leu
      50      55      60

```

20250220 14:43:43

Gly Lys Met Lys Val Ser Ala Leu Leu Glu Ala Leu Pro Lys Val Gly
 65 70 75 80
 Lys Val Lys Ala Gln Glu Ile Met Thr Glu Leu Glu Ile Ala Pro His
 85 90 95
 Pro Ala Ala Phe Val Ala Ser Val Thr Val Ser Ala Arg Pro Cys Trp
 100 105 110
 Lys Ser Ser Ala Pro Pro Asn Pro Ala Gly Arg Arg Cys Gly Pro Glu
 115 120 125
 Gly Leu Trp Trp Ala Tyr Pro Arg Ile Arg Gly Arg Ser Gly Leu Thr
 130 135 140
 Gly Pro Ala His Asn Ser Gly Arg Thr Pro Arg Trp Gly Gly Thr Arg
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Asp Trp His Arg Gln Pro Pro His Arg Gly Arg Ala Asp Gln His Leu
 1 5 10 15
 Gly Leu Asp Ala Arg Leu Cys Ala Ala Ala Cys Asn Val Leu Leu Val
 20 25 30
 Asp Gly Val Gln His Arg Pro Gln Arg His Gly Pro Gly Pro Arg Phe
 35 40 45
 Gly Phe Pro Arg Val Val Val Ala Cys Gly Ile Arg Gln Ala Arg Val
 50 55 60
 Glu Val Glu Arg Phe Gly Gly Val Val Pro Glu Arg Ala His Gly Val
 65 70 75 80
 Gly Gln Arg Asn Asn Arg Val Ala Thr Asp Arg Leu Thr Asp Arg Met
 85 90 95
 Pro Ile Asp Arg Gly Leu Gly Arg Glu Pro Arg Ser Val Gly Gly Gln
 100 105 110
 Ile Asp Arg Glu Arg Asp Gln Pro Gln Arg Ile Pro Ala Gly Lys His
 115 120 125
 Val Thr Pro His Cys Pro Gln Pro Arg Ser Leu His Leu Val Leu Thr
 130 135 140
 Ser Arg Arg His Val Glu Arg Gln Arg His Arg Ala Glu Glu Gln His
 145 150 155 160
 Glu Val His Ala Gly Pro Leu Gly Gly Ala Ser Gln Ser Gln Ala Ala
 165 170 175
 Pro Arg

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: nucleic acid

20250204 09:44:43

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237: ..

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ATGCCAAGCC | GGTGCTGATG | CCCGAGCTCG | GCGAATCGGT | GACCGAGGGG | ACCGTCATTC | 60 |
| GTTGGCTGAA | GAAGATCGGG | GATTCGGTTC | AGGTTGACGA | GCCACTCGTG | GAGGTGTCCA | 120 |
| CCGACAAGGT | GGACACCGAG | ATCCCGTCCC | CGGTGGCTGG | GGTCTTGGTC | AGTATCAGCG | 180 |
| CCGACGAGGA | CGCCACGGTG | CCCGTCGGCG | GCGAGTTGGC | CCGGATCGGT | GTCGCTGCCG | 240 |
| AGATCGGCGC | CGCGCCCGCC | CCCAAGCCCC | C | | | 271 |

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Lys | Pro | Val | Leu | Met | Pro | Glu | Leu | Gly | Glu | Ser | Val | Thr | Glu | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Thr | Val | Ile | Arg | Trp | Leu | Lys | Lys | Ile | Gly | Asp | Ser | Val | Gln | Val | Asp |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Glu | Pro | Leu | Val | Glu | Val | Ser | Thr | Asp | Lys | Val | Asp | Thr | Glu | Ile | Pro |
| | | | 35 | | | | | 40 | | | | | 45 | | |
| Ser | Pro | Val | Ala | Gly | Val | Leu | Val | Ser | Ile | Ser | Ala | Asp | Glu | Asp | Ala |
| | | | 50 | | | | | 55 | | | | | 60 | | |
| Thr | Val | Pro | Val | Gly | Gly | Glu | Leu | Ala | Arg | Ile | Gly | Val | Ala | Ala | Glu |
| 65 | | | | | | 70 | | | | 75 | | | | | 80 |
| Ile | Gly | Ala | Ala | Pro | Ala | Pro | Lys | Pro | | | | | | | |
| | | | | | | 85 | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAGGTAGCGG | ATGGCCGGAG | GAGCACCCCA | GGACCGCGCC | CGAACCGCGG | GTGCCGGTCA | 60 |
| TCGATATGTG | GGCACCGTTC | GTTCCGTCCG | CCGAGGTCAT | TGACGAT | | 107 |

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

```

ATGAAGTTGA AGTTTGCTCG CCTGAGTACT GCGATACTGG GTTGTGCAGC GCGCCTTGTG      60
TTTCCTGCCT CGGTTGCCAG CGCAGATCCA CCTGACCCGC ATCAGCCGGA CATGACGAAA      120
GGCTATTGCC CGGGTGGCCG ATGGGGTTTT GGCGACTTGG CCGTGTGCGA CGGCGAGAAG      180
TACCCCGACG GCTCGTTTTG GCACCAAGTG ATGCAAACGT GGTTCACCGG CCCACAGTTT      240
TACTTCGATT GTGTCAGCGG CGGTGAGCCC CTCCCCGGCC CGCCGCCACC GGGTGGTTGC      300
GGTGGGGCAA TTCCGTCCGA GCAGCCCAAC GTCCTCTGA                               339

```

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

```

Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala
 1           5           10           15
Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp
 20           25           30
Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp
 35           40           45
Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly
 50           55           60
Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe
 65           70           75           80
Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro
 85           90           95
Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln Pro Asn Ala Pro
100           105           110

```

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

209220" E484300T

GTGACCACGG TGGGCCTGCC ACCAACCCGG GCAGCGGCAG CCGCGGCGGC GCCGGCGGCT 60
 CCGGCGGCAA CGGTGGCGCC GGGGGTAACG CCACCGGCTC AGGCGGCAAG GGCGGCGCCG 120
 GTGGCAATGG CGGTGATGGG AGCTTCGGCG CTACCAGCGG CCCC GCCTCC ATCGGGGTCA 180
 CGGGCGCCCC CGGCGGCAAC GCGGCAAGG GCGGCGCCGG TGGCAGCAAC CCCAACGGCT 240
 CAGGTGGCGA CGGCGGCAAA GCGGCAACG GCGGTGCCGG CCGCAACGGG GGCTCGATCG 300
 GCGCCAACAG CGGCATCGTC GCGGTTCCG GTGGGGCCGG TGGCGCTGGC GGCGCCGGCG 360
 GAAACGGCAG C 371

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

GTCCGGGTCC CACCACCGCG CCGGCGCGCC CCTAGCGGCC GGGCGCACCA GCCCCTTTTC 60
 TTGACTCGTT CAAGAAAAGG GCCTTCTGTT TGGTCGGCCA TGTGTCATG ATCGTGACCC 120
 ATGGGCAACA TCGACGTCGA CATCTCGGCC AAGGTCTAGC TCCATGCGAA TCGCCGCCGC 180
 GGTGGTGAGC ATCGGTCTAG CCGTCATAGC AGGGTTCGCG GTACCTGTTG CCGACGCACA 240
 CCCGTCGGAG CCCGGGGTTG TGTCTACGC GGTGCTCGGA AAGGGGTCGG TCGGCAACAT 300
 CGTCGGCGCC CCAATGGGGT GGGAGGCGGT GTTCACCAAG CCGTCCAGG CGTTTTGGGT 360
 CGAACTACCG GCGTGCAACA ACTGGGTGGA CATCGGGCTG CCCGAGGTGT ACGACGATCC 420
 CGAC 424

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

GCGATGGCGG CCGCGGGTAC CACCGCCAAT GTGGAACGGT TTCCCAACCC CAACGATCCT 60
 TTGCATCTGG CGTCAATTGA CTTCAGCCCC GCCGATTTCG TCACCGAGGG CCACCGTCTA 120
 AGGGCGGATG CGATCCTACT GCGCCGTACC GACCGGCTGC CTTTCGCCGA GCCGCCGGAT 180
 TGGGACTTGG TGGAGTCGCA GTTGCGCACG ACCGTCACCG CCGACACGGT GCGCATCGAC 240
 GTCATCGCCG ACGATATGCG TCCCGAACTG GCGGCGGCGT CCAAATCAC CGAATCGCTG 300
 CGGCTCTACG ATTCGTC 317

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TGGCGTATGC | GCTTCGCAGC | CGGTGCCGCG | TCAACGCGCC | GGAGGCAATC | GCTTCGCTGC | 60 |
| CGAGGAATGG | TTCGATCACG | ATCGCAGTGT | GCCGTCGTGC | ACCGACACCG | CCGTCCAACG | 120 |
| TGAACTGAGG | GCGGAAAATC | GGCCGAAATC | TCGCCCTCAG | TTCACGCTCG | GCGCCTAACG | 180 |
| GTTCTGGAAG | TTGGGTGCGC | GCTTCTCGGC | GAACGCGCGC | GGGCCTTCCT | TGGCGTCGTC | 240 |
| GGACAGGAAG | ACCTTGATGC | CGATCTGGGT | GTCGATCTTG | AACGCCTCGT | TTTCGGGCAT | 300 |
| GCACTCGGTC | TCGCGGATGG | ACCGCAAGAT | GGCCTGCACG | GCCAGGGGTC | CGTTAGCCGA | 360 |
| GATGGCGTCG | GCAAGTTCTA | GAACCTTGGT | CAACGCCTGG | CCGTCGGGCA | CACGTGGCCG | 420 |
| AT | | | | | | 422 |

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGGTGCCGCT | GAACACCAGC | CCGCGGCTGC | CAGATCTCCC | GGACTCGGTA | GTGCCGCCGG | 60 |
| TGGCGTCGTT | GCTCTCCTGA | CGGGGCGCGG | CGACCATAAG | GTCGCTAATG | CCCAGGTAGC | 120 |
| GGCCCAGGTG | CATGGAGTCG | ATGATGATGC | GACTCTCCAG | CTCGCCGACC | GGGAGCTTGG | 180 |
| CATCGGGCCT | GATCAGCCAG | GACGCGTAGG | ACAAGTCGAT | CGAATGCATA | GTGGCCTCCA | 240 |
| GAGTGGCCGT | GCCACTTCCG | GCGTGCTCCA | CGGCAAATGC | CTTGATTCT | AGTCCGCGT | 300 |
| AGTGTTCCCG | CATCGCCTGC | GGGATGAATG | GGAACCGCAG | GATGGCGACA | AACGGGTCTG | 360 |
| ACCTCAGGTT | TGCCGCTTTG | CGCACAGTGG | TCGACAGCCG | GTAATCGGCA | TAAATGCTGG | 420 |
| CCCCGA | | | | | | 426 |

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AGACCGGCGA | GGGTGTGGTC | GCTGCCCGCG | GCATTGTGCA | TAATCTGCGC | TGGGTGACG | 60 |
| CGCCGATCAA | CTAGTGAGGC | GCAACGCTAG | GCTTTGGGAT | ACCCACAGCT | AAAAAGTTTA | 120 |
| TCAAAGAAAC | GAAGAAGGTT | GCCATGAGCA | CTGTTGCCGC | CTACGCCGCC | ATGTCGGCGA | 180 |
| CCGAACCCCT | GACCAAGACC | ACGATACCCC | GTCGCGACCC | GGGCCCCGAC | GACATGGCGA | 240 |
| TCGACATCAA | ATTTCGCCGA | ATCTGTCGCT | CGGACATCCA | TACCGTCCAA | ACCGAATGGG | 300 |
| GGCAACCGAA | TTTACCTGTG | GTCCCTG | | | | 327 |

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

```

Asp His Gly Gly Pro Ala Thr Asn Pro Gly Ser Gly Ser Arg Gly Gly
 1          5          10          15
Ala Gly Gly Ser Gly Gly Asn Gly Gly Ala Gly Gly Asn Ala Thr Gly
 20          25          30
Ser Gly Gly Lys Gly Gly Ala Gly Asn Gly Gly Asp Gly Ser Phe
 35          40          45
Gly Ala Thr Ser Gly Pro Ala Ser Ile Gly Val Thr Gly Ala Pro Gly
 50          55          60
Gly Asn Gly Gly Lys Gly Gly Ala Gly Gly Ser Asn Pro Asn Gly Ser
 65          70          75          80
Gly Gly Asp Gly Gly Lys Gly Gly Asn Gly Gly Ala Gly Gly Asn Gly
 85          90          95
Gly Ser Ile Gly Ala Asn Ser Gly Ile Val Gly Gly Ser Gly Gly Ala
100          105          110
Gly Gly Ala Gly Gly Ala Gly Gly Asn Gly Ser
115          120

```

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

```

Met Ala Ala Ala Gly Thr Thr Ala Asn Val Glu Arg Phe Pro Asn Pro
 1          5          10          15
Asn Asp Pro Leu His Leu Ala Ser Ile Asp Phe Ser Pro Ala Asp Phe
 20          25          30
Val Thr Glu Gly His Arg Leu Arg Ala Asp Ala Ile Leu Leu Arg Arg
 35          40          45
Thr Asp Arg Leu Pro Phe Ala Glu Pro Pro Asp Trp Asp Leu Val Glu
 50          55          60
Ser Gln Leu Arg Thr Thr Val Thr Ala Asp Thr Val Arg Ile Asp Val
 65          70          75          80
Ile Ala Asp Asp Met Arg Pro Glu Leu Ala Ala Ala Ser Lys Leu Thr
 85          90          95
Glu Ser Leu Arg Leu Tyr Asp Ser
100

```

205220" E4348001

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ser | Thr | Val | Ala | Ala | Tyr | Ala | Ala | Met | Ser | Ala | Thr | Glu | Pro | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Thr | Lys | Thr | Thr | Ile | Thr | Arg | Arg | Asp | Pro | Gly | Pro | His | Asp | Met | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ile | Asp | Ile | Lys | Phe | Ala | Gly | Ile | Cys | Arg | Ser | Asp | Ile | His | Thr | Val |
| | | 35 | | | | | 40 | | | | | 45 | | | |

Gln Thr Glu Trp Gly Gln Pro Asn Leu Pro Val Val Pro
50 55 60

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| GCTTGGAGCC | CTGGAGCGAC | GGTGTGGGTC | TGGGGGTCGA | TTCGTTCTCG | GCGAAAGTCA | 60 |
| ACTAAAGACC | ACGTTGACAC | CCAACCGGCG | GCCCCGGCATG | GGCCGTCGCG | GCGTAGAAGC | 120 |
| TTTGACCGCG | GCGCGAAACG | TTCGCTGCTG | CGGCCCATGC | AGATCGCACA | CGCTTGCTTG | 180 |
| AACATCGGGT | GGAGCCGGTG | GTAACGCCAG | GCT | | | 213 |

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| CCGAGCTGCT | GTTCGGCGCC | GGCGGTGCGG | GCGGCGCGGG | TGGGGCGGGC | ACCGACGGCG | 60 |
| GGCCCCGGTGC | TACCGGCGGG | ACCGGCGGAC | ACGGCGGAGT | CGGCGGCGAC | GGCGGATGGC | 120 |
| TGGCACCCCG | CGGGGCCGGC | GGGGCCGGCG | GGCAAGGCGG | GGCAGGTGGT | GCCCCGAGCG | 180 |
| ATGGTGGCGC | GTTGGGTGGT | ACCGGCGGGA | CGGGCGGTAC | CGGCGGCGCC | GGTGGCGCCC | 240 |
| GCGGTGCGCG | CACACTGCTG | CTGGGCGCTG | GCGGACAGGG | CGGCCTCGGC | GGCGCCGGCG | 300 |
| GACAAGGCGG | CACCGGCGGG | GGCCGGCGGA | GATGGCGTTC | TGGGGGGTGT | CAGTGGCACT | 360 |
| GGTGGTA | | | | | | 367 |

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| AAGGCGTGAT | TGGCAAGGCG | ACCGCGCAGC | GGCCCCGTAGC | CGCGGGACGG | CCCAGGCCCC | 60 |
| GACCGCAGCG | GCCGGTGTCT | GACCGGGTCA | GCGACCAGCG | GCGCTGACCG | TGCCGCTCGT | 120 |
| CTACTTCGAC | GCCAGCGCCT | TCGTCAAAC | TCTCACCACC | GAGACAGGGA | GCTCGCTGGC | 180 |

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GTCCGCTCTA TGGGACGGCT GCGACGCCGC ATTGTCCAAC CGCCTGGCCT ACCCCGAAGT 240
 CCGCGCCGCA CTCGCTGCAA CGGGCCGCAA TCACGACCTA ACCGAATCCG AGCTCGCCGA 300
 CGCCGAGCGT GACTGGGAGG ACTTCTGGGC CGCACCCGCC CAGTCGAACT CACCGCGACG 360
 GTTGAACAGC ACGCCGGGCA CCTCGCCCGA ACACATGCCT TACGCGGAGC CGACACCGTT 420

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

CTCTTGTCGG TGGCATCGGC GGTACCGGCG GAACCGGCGG CAACGCCGGT ATGCTCGCCG 60
 GCGCCGCCGG GGCCGGCGGT GCCGGCGGGT TCAGCTTCAG CACTGCCGGT GGGGCTGGCG 120
 GCGCCGGCGG GGCCGGTGGG CTGTTACCA CCGGCGGTGT CGGCGGCGCC GGTGGGCAGG 180
 GTCACACGGG CGGGGCGGGC GGCGCCGGCG GGGCCGGCGG GTTGTGTTGGT GCCGGCGGCA 240
 TGGGCGGGGC GGGCGGATTC GGGGATCACG GAACGCTCGG CACCGGCGGG GCCGGCGGG 299

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Leu Glu Pro Trp Ser Asp Gly Val Gly Leu Gly Val Asp Ser Phe Ser
 1 5 10 15
 Ala Lys Val Asn
 20

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Glu Leu Leu Phe Gly Ala Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly
 1 5 10 15
 Thr Asp Gly Gly Pro Gly Ala Thr Gly Gly Thr Gly Gly His Gly Gly

20 25 30
 Val Gly Gly Asp Gly Gly Trp Leu Ala Pro Gly Gly Ala Gly Gly Ala
 35 40 45
 Gly Gly Gln Gly Gly Ala Gly Gly Ala Arg Ser Asp Gly Gly Ala Leu
 50 55 60
 Gly Gly Thr Gly Gly Thr Gly Gly Thr Gly Gly Ala Gly Gly Ala Gly
 65 70 75 80
 Gly Arg Gly Thr Leu Leu Leu Gly Ala Gly Gly Gln Gly Gly Leu Gly
 85 90 95
 Gly Ala Gly Gly Gln Gly Gly Thr Gly Gly Gly Arg Arg Arg Trp Arg
 100 105 110
 Ser Gly Gly Cys Gln Trp His Trp Trp
 115 120

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

Gly Val Ile Gly Lys Ala Thr Ala Gln Arg Pro Val Ala Ala Gly Arg
 1 5 10 15
 Pro Arg Pro Arg Pro Gln Arg Pro Val Ser Asp Arg Val Ser Asp Gln
 20 25 30
 Arg Arg

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

Leu Val Gly Gly Ile Gly Gly Thr Gly Gly Thr Gly Gly Asn Ala Gly
 1 5 10 15
 Met Leu Ala Gly Ala Ala Gly Ala Gly Gly Ala Gly Gly Phe Ser Phe
 20 25 30
 Ser Thr Ala Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly Gly Leu Phe
 35 40 45
 Thr Thr Gly Gly Val Gly Gly Ala Gly Gly Gln Gly His Thr Gly Gly
 50 55 60
 Ala Gly Gly Ala Gly Gly Ala Gly Gly Leu Phe Gly Ala Gly Gly Met
 65 70 75 80

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Gly Gly Ala Gly Gly Phe Gly Asp His Gly Thr Leu Gly Thr Gly Gly
 85 90 95
 Ala Gly Gly

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

| | | | | | | |
|-------------|------------|------------|------------|-------------|------------|-----|
| TCCTGTTTCGG | CGCCGGCGGG | GTGGGCGGTG | TTGGCGGTGA | CGGTGTGGCA | TTCCTGGGCA | 60 |
| CCGCCCCCGG | CGGGCCCGGT | GGTGCCGGCG | GGGCCGGTGG | GCTGTTTCAGC | GTCGGTGGGG | 120 |
| CCGGCGGCGC | CGGCGGAATC | GGATTGGTCG | GGAACAGCGG | TGCCGGGGGG | TCCGGCGGGT | 180 |
| CCGCCCTGCT | CTGGGGCGAC | GGCGGTGCCG | GCGGCGCGGG | TGGGGTCGGG | TCCACTACCG | 240 |
| GCGGTGCCGG | CGGGGCGGGC | GGCAACGCCA | GCCTGCTGGT | AA | | 282 |

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGGCACGAGC | CGTGCTACTG | GTCAACTGAT | GCCCTGATTG | TGACCTTCCC | GGCGCCGGAT | 60 |
| CAGTGCTTCT | CAGGACCGAC | GTAATATTCG | AAAACCAATC | CGGCCGCCGA | GGCGAGGATG | 120 |
| AATGCCACAC | CGGCGGCGAT | CAGCCACGGG | AGCCACAACG | CGATGCCGAC | CGCTGCCACC | 180 |
| GAGCCGGACA | ACGCGACCAT | GATCGGCCAC | CAGCTATGCG | GAAGAAGAA | TCCAAGTTCT | 240 |
| CCTGCGCCGT | CGCTGATTTC | AGCGCCTTCG | TAGTCCTCGG | GCCGGAATC | TAACCGGCGG | 300 |
| GCCACAAACC | GGAAGAAGGT | GGCGACGATC | AACGCCATGC | CGCCGGTGAG | CGCCAACGCA | 360 |
| ATGGTGCCAG | CCCACTCGAC | ACCACCGGTG | GCGAACATCG | AGGTCAACAC | GCCGT | 415 |

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

| | |
|---|-----|
| TCACCGCGTG AACGGTTCGT AACACTGATA CGTATGCTTG TCAGCGAGCA GATCAAGTCC | 60 |
| AGTCCGACCA ATGCCAGGAG ATCATCGGCT AGGCTCACGG TTTCGCCTGG GACGAGACGG | 120 |
| TATTGAGTTC TGGCGTTGGA CGGTCCGTGG CGTGGTGGGA AGTCTGACGC GGCATCAGAA | 180 |
| CGGTTGTCAA TACCAGTCTT TGGGGGATAT GGCCTATTTG GTGTCGTCGG GCCGCTCCAC | 240 |
| CGGATCCCTT TTCGAACGTT GCGCAAGCGC GGTCCAGTTA CGGCCTGTTC ACTGCGCGCT | 300 |
| GGCGTAGCTG CGCGGCCTCG ATCGGTTTGA ACGTCATCGC AATTCCCGCA ATGGGTGAGT | 360 |
| ACCTGACGCT CCT | 373 |

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

| | |
|---|-----|
| CCAAACCGGA CAGGCCGGCA GCGACGGTCG GAAGTTGCAC CACGGTGCGC GCTCCATGTA | 60 |
| GCCAACCGGT GACCACGGCG TAGACAGCAG ATCCGTGGAT CGCGCGTTTC GTGTCGTCCG | 120 |
| GGCCGAGTAC CCGCGGGCCG AACCAGCGC ACCAAAGCAA CGCGATCGAT ACGGGGATCG | 180 |
| CCACTCGTGC CGAATTCGAG CTCCGTGCAC AAGCTTGCGG CCGCACTCGA ACCCGGGTGA | 240 |
| ATGATTGAGT TTAAACCGCT TAGCAATAAC TAGCATAACC CCTTGGGGCC TCTAAACGGG | 300 |
| TCTTGAGGGG TTTTTTGCTG AAAGGAGGAA CTATATCCGG ATAACCTGGC GTAGTAGCGA | 360 |
| AGAGGCCCCG ACCGATCGCC CTTCCCAACA GTTGCGCAGC CTGAATGGCG AATGGACGCG | 420 |
| CCC | 423 |

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

| | |
|--|-----|
| AGTGGCCAGC CGGTGGGCCA ATGCATCCAG CTCCCGGTAC GTCAGCTGAC CATCCGCCCCA | 60 |
| ACTGACCGCC ACCGAGTCAG GCTGTGCCGC AGCGATTTTC GCGAACCAGG TATGCACCGC | 120 |
| GGGTGCCGAC GTCGTCACAT CCGGCAGGCC GGGTGCGGTC GGATCGTGCT CGCCGTCCAG | 180 |
| CAGAATGTCG ACGTCGCGCA GCGGCCGATC CCACCGGCTG ACCAAGCGCT GTAACACAGC | 240 |
| CAGCACCCGC CTGCCGAGGC TTTCGGGCGC CATCGTGCCC AGCGCACCGT CGAGCACCTC | 300 |
| CACTAGCAGC GTGAGCTCAC CGGTGCTGCG GTGCGCGGCG ACGGTCACCG GAAAGTGCGA | 360 |
| CAAACCTCTCT AGCGCCACCG GACGGAACGT CACCCCGTTT GCGA | 404 |

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTCCTGGTCG | CAGGCTGTTC | TTCGAACCCG | CTGGCTAACT | TCGCACCCGG | GTATCCGCCC | 60 |
| ACCATCGAAC | CCGCCCAACC | GGCGGTGTCA | CCGCCTACTT | CGCAAGACCC | GGCCGGTGCA | 120 |
| GTGCGACCAC | TGAGCGGCCA | CCCCGGGGCG | GCACTATTCT | ACAACGGCAC | CCGCCAATTG | 180 |
| GTGGCTCTGC | GCCCCGGGCG | CGATTCGGCG | GCACCCGCCA | GCATCATGGT | CTTCGATGAC | 240 |
| ATGCACGTTG | CACCGCGCGT | CATTTTCTCT | CCGGGCCCCG | CAGCCGCGTT | GACCAGCGAC | 300 |
| GACCACGGCA | CGGCCTTCCT | TGCCGCCCCG | GGCGGCTACT | TCGTGGCCGA | CCTGTCCTCC | 360 |
| GGTCACACCG | CACGAGTGAA | TGTCGCTGAC | GCAGCGCACA | CCGATTTCAC | CGCGATCGCC | 420 |
| C | | | | | | 421 |

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

| | | | | | | |
|------------|-------------|------------|------------|------------|-------------|-----|
| ATGCATATCA | CGCTCAACGC | CATCCTGCGT | GCGATCTTCG | GGGCCGGCGG | CAGTGAACCTA | 60 |
| GACGAGCTGC | GCCGCCTCAT | TCCGCCGTGG | GTCACGCTGG | GCTCGCGCCT | GGCGGCGCTA | 120 |
| CCGAAACCCA | AACGCGACTA | TGGCCGCCTT | AGCCCGTGGG | GCCGGCTGGC | CGAGTGGCGG | 180 |
| CGCCAGTACG | ACACTGTTCAT | CGACGAGCTC | ATCGAAGCCG | AGCGGGCCGA | CCCGAACTTC | 240 |
| GCCGATCGGA | CCGACGTTTT | GGCGTTGATG | CTGCGCAGCA | CTTACGACGA | CGGTTCCATC | 300 |
| ATGTCGCGCA | AGGACATTGG | CGACGAACTG | CTCACGCTGC | TTGCCGCCGG | GCACGAAACC | 360 |
| ACGGCGGCGA | CATGGGCTGG | GCGTTCGAAC | GGCTCAACCG | GCACCCCGAC | GTGCTCGCGG | 420 |
| CTCTGG | | | | | | 426 |

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTCCTGGTCG | CAGGCTGTTC | TTCGAACCCG | CTGGCTAACT | TCGCACCCGG | GTATCCGCCC | 60 |
| ACCATCGAAC | CCGCCCAACC | GGCGGTGTCA | CCGCCTACTT | CGCAAGACCC | GGCCGGTGCA | 120 |
| GTGCGACCAC | TGAGCGGCCA | CCCCGGGGCG | GCACTATTCT | ACAACGGCAC | CCGCCAATTG | 180 |
| GTGGCTCTGC | GCCCCGGGCG | CGATTCGGCG | GCACCCGCCA | GCATCATGGT | CTTCGATGAC | 240 |
| GTGCACGTTG | CACCGCGCGT | CATTTTCTCT | CCGGGCCCCG | CAGCCGCGTT | GACCAGCGAC | 300 |
| GACCACGGCA | CGGCCTTCCT | TGCCGCCCCG | GGCGGCTACT | TCGTGGCCGA | CCTGTCCTCC | 360 |
| GGTCACACCG | CACGAGTGAA | TGTCGCTGAC | GCAGCGCACA | CCGATTTCAC | CGCGATCGCC | 420 |

CGCCGCTCCG ACGGCAAGCT GGTGCTGGGC AGCGCAGATG GCGCCGTCTA CACGCTTGCC 480
AAGAACCCGC AGTTGACCGG CGTCGGCGCC GCCACCGTAG CC 522

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| GCTGGGGCGC | ACCGCCGTCC | GGCGGCCCCA | GCCCCTGGGC | CCAGACCCCG | CGCAAAACCA | 60 |
| ACCCGTGGCC | CTTAGTGGCC | GGCGCCGCGC | CCGTCTGTCT | CGTCCTCGTG | TTGGGCGCCA | 120 |
| TCGGCATCTG | GATCGCCATC | CGGCCCCAAGC | CGGTACAGCC | GCCTCAGCCG | GTTCGGGAGG | 180 |
| AGCGCCTTAG | CGCCCTACTG | CTGAAGTCTC | CAGAAGTCAA | CGCCGTGATG | GGCTCGTCGT | 240 |
| CCATGCAGCC | GGGCAAACCG | ATCACATCGA | TGGACTCTTC | GCCGCTGACG | GTGTCCCTGC | 300 |
| CGGACTGCCA | GGGCGCGCTG | TATACCAGCC | AGGATCCGGT | GTATGCCGGC | ACCGGCTACA | 360 |
| CCGCCATCAA | CGGCTTGATT | TCATCCGAGC | CGGGCGACAA | CTACGAACAT | TGGGTGAACC | 420 |
| AAGCCGTCTG | CGCCTTTCCG | ACCGCCGACA | AAGCCGCGC | GTTCGTGCAG | ACTTCGGCCG | 480 |
| ACAAATGGAA | GAAGTGCACA | GGCAAGACGG | TCACCGTCAC | GAATAAGGCC | AAGACCTACC | 540 |
| GGTGGACGTT | TGCCGACGTC | AAAGGCAGCC | CGCCGACGAT | CACGGTGATA | GACACCCAAG | 600 |
| AAGGCGCTGA | GGGCTGGGAA | TGCCAACGCG | CGATGAGCGT | GGCCAACAAT | GTGGTTGTCT | 660 |
| ACGTCAACGC | ATGCGGGTAC | CAGATCACCA | ATCAAGCAGG | CCAGATCGCC | GCCAAGATCT | 720 |
| GTTGACAAAG | TCAACAAGG | | | | | 739 |

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|----|
| AGACGTCGTC | GAGGCCGCCA | TCGCCCAGCG | CGAAGCCGTT | AACCCGGCAC | TGAACGCGTT | 60 |
| GGCGTATGC | | | | | | 69 |

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

ACTGCACCCG GCAGGCGCGA CCAACGGATC GGGTCAACTA GCACTGCCGG TGGAGGCGCC 60
 CCCGCGGTCT GTGCCTTCCC ACGGGGAACC CTTGGGCAGC GCGGCTCCAG AAGGGTTGGA 120
 GGGAGAGTTC GACGACCGTA TCGACGAGCG GTTCCCGGTC TTCAGCTCGG CCAGTCTCGC 180
 CGAAGCGCTG CCGGGTCCGC TGACCCCGAT GACGCTGGAT GTCCAGTTGA GTGGACTGCG 240
 CGCGGCCGGT CGGGCGATGG GTCGGGTACT GCGCTTGGC GGTGTCGTTG CCGATGAGTG 300
 GGAGAGAAGA GCCATCGCGG GTTTCGGTCA CCGCCGTAT ATCGGAGTGT CGGCCAATAT 360
 TGTGGCCGCC GCCCAACTGC CGGGGTGGGA CGCGCAGGCC GTAACCCGGC GGGCACTGGG 420
 CGAGCAACCG CAGGTCAC TGCTGCTTCC GTTTGGTCGA CCGCAACTTG CGGGCGGACC 480
 GCTCGGCTCG GTCGCGAAGG TGGTCGTGAC GGCACGGTCG CTG 523

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

GTGTCGGTGT CGTCGGGGTA GGAGCGACTT CCCCGGCCGG CGCCGGCGCC GGAGCGGGCT 60
 CTGCAGGAAC CGGTGCCGGC GCCGGCGGCG GGGCGACCAA AGGCCGGATC GATTTCGGCCA 120
 GCGCCTTGGC CGCGCCCTTG TCCACCGGT GTTTGGCGGT CCCGAGCCAT ACCACAAACC 180
 AACGCTGAAG GGGCCCGGCG TCCGGTGCGT TCGCCGCGGG CGAC 224

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

TGAACTGACT GCGCCGCTCG ATCGGCGGCG GCGGCGTGTC ATAGCTGCGC CGCCAGGCCA 60
 TGAACTGCTC TTCGCCATAG CGGGCCTTGG TCTCGGCCTT GTCCAAACCC TGCAGCGCGC 120
 CGTAGTGGCG TTCGTTGAGC CGCCAGCTAC GCCGCACGGG AATCCAGAGC CGATCGGCGC 180
 TGTCCAACGC CAGATGCGCG GTGGTGATCG CGCGCCGCGC CAACGAGGTG TAGAGCACGT 240
 CGGGCAATAG GTCGTGTTCC GCGATCAGCT CGCCGCTTCG AACCGCCTCT GCCTGGCCCT 300
 TGTCCGTCAG GCCGACATCG ACCAGCCGG TGAACAGGTT GAGGGCATTC CAGTCGCTCT 360
 CGCCGTGGCG CAGCAACACC AGGCTGCCAG TGTTCGCCAT ACCGGCAAGT CTCTCACGCA 420
 CTCCGCACT CCTCATCGTG GACCAAAATG CCCGAATTCT CCTCGGTCCG CTGCGCAGCG 480
 CGTTCATACC GCCGAGGTGG TCGGCACCGT AACGGCCGGT T 521

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| CTCCAGGCTC | ATTGCTCGA | ACAAAGCCAC | CCGGCCGTAC | AGCGGACGCC | CCCATTTCGTT | 60 |
| GTCGTGATAG | TCGCGGTACA | GCTGGGCATC | GGGCCCTGGA | CGAACCTCCG | CCCAGGGGCA | 120 |
| GCGAACCAGC | CCGTCGCCGC | TCACGCGGGG | TCAGAACGGT | AGTGCACGAC | AGTCTCGCCG | 180 |
| CGCGAAGGGT | TTGACGCGTC | AGACTCGGCC | TCGGCGTCTT | CCGACGAGGC | GTGGATCGCC | 240 |
| CCGAGCTGAG | AGCGTAGCGC | CTCGAGCTCA | CGGCCGAGCC | GTTCCAGCAC | CCAGTCCACC | 300 |
| TCGCTGGTCT | TGTTCCCGCG | CAGCACCTGC | GTGAACTTGA | CCGCGTCGAC | ATCGGC CGCG | 360 |
| GTGACCCCGA | ACGCCGGCAG | CGTCGTCGCC | GTCGTCGCC | GCGGCAGGGG | CGGCAACTGC | 420 |
| TCGCCA | | | | | | 426 |

(2) INFORMATION FOR SEQ ID NO:275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCGGACACGG | CGGACAAAGC | GCAATCGGCC | TCGGCGGCGG | CGCCGGCGGC | GACGGGGGCC | 60 |
| AGGGCGGCGC | CGGCCGCGGA | CTGTGGGGTA | CTGGCGGCGC | CGGCGGACAC | GGCGGGGCAA | 120 |
| GGCGGTGGTA | CCGGGGGCC | ACCGTGCC | GGTCAGGCAG | GCATGGGCGC | CGCGGGTGGC | 180 |
| GCCGGTGGGC | TGATCGGCAA | CGGCGGGGCC | GGCGGCGAC | | | 219 |

(2) INFORMATION FOR SEQ ID NO:276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

| | | | | | | |
|-------------|------------|-------------|------------|------------|------------|-----|
| AAGATCATCG | GCGCCGCTCC | TTAGCATCGC | TGCGCTCTGC | ATCGTCGCCG | GCGCGGATCA | 60 |
| CGGAGGTCCG | GCCTTGTAAC | CCACTCCTCG | AACGGTCAGC | ACCACAGTCG | GGTTCTCGGG | 120 |
| ATCCTTTTCG | ACCTTGCCCC | GCAGACGCTG | GACATGCACG | TTCACCAGCC | TGGTATCGGC | 180 |
| TGGGTGCCGG | TAACCCATA | CCTGTTTCGAG | CAGCACATCA | CGAGTAAACA | CCTGGCGCGG | 240 |
| CTTGCGCGCC | AATGCGACCA | ACAGGTCGAA | TTCCAGCGGT | GTCAACGAGA | TCTGCTCACC | 300 |
| GTTGCGAGTG | ACCTTGTCG | CCGGTACGTC | GATTTCTACG | TCGGCGATGG | ACAGCATCTC | 360 |
| GGCGGGTTTCG | TCGTCGTTGC | GGCGCAGCCG | CGCCCGCACC | CGCGCAACCA | GCTCCTTGGG | 420 |
| CTTGAACGGC | TTCATGATGT | AGTCGTCGGC | GCCCCACTCC | AGACCCAGCA | CCACATCCAC | 480 |
| GGTGTCGGTC | TTTGCGGTGA | GCATCACGAT | CGGAACACCG | GAATCGGCGC | GCAACACCCG | 540 |
| GCACACGTCG | ATGCCGTTCA | TACCGGGGCA | A | | | 571 |

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

```

Leu Phe Gly Ala Gly Gly Val Gly Gly Val Gly Gly Asp Gly Val Ala
 1           5           10           15
Phe Leu Gly Thr Ala Pro Gly Gly Pro Gly Gly Ala Gly Gly Ala Gly
      20           25           30
Gly Leu Phe Ser Val Gly Gly Ala Gly Gly Ala Gly Gly Ile Gly Leu
      35           40           45
Val Gly Asn Ser Gly Ala Gly Gly Ser Gly Gly Ser Ala Leu Leu Trp
      50           55           60
Gly Asp Gly Gly Ala Gly Gly Ala Gly Gly Val Gly Ser Thr Thr Gly
65           70           75           80
Gly Ala Gly Gly Ala Gly Gly Asn Ala Ser Leu Leu Val
      85           90

```

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```

Met Pro Pro Val Ser Ala Asn Ala Met Val Pro Ala His Ser Thr Pro
 1           5           10           15
Pro Val Ala Asn Ile Glu Val Asn Thr Pro
      20           25

```

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

205220" E484800T

Lys Pro Asp Arg Pro Ala Ala Thr Val Gly Ser Cys Thr Thr Val Arg
 1 5 10 15
 Ala Pro Cys Ser Gln Pro Val Thr Thr Ala
 20 25

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Trp Pro Ala Gly Arg Pro Met His Pro Ala Pro Gly Thr Ser Ala Asp
 1 5 10 15
 His Pro Pro Asn
 20

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro
 1 5 10 15
 Gly Tyr Pro Pro Thr Ile Glu Pro Ala Gln Pro Ala Val Ser Pro Pro
 20 25 30
 Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro
 35 40 45
 Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg
 50 55 60
 Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp
 65 70 75 80
 Met His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala
 85 90 95
 Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly
 100 105 110
 Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val
 115 120 125
 Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala
 130 135 140

(2) INFORMATION FOR SEQ ID NO:282:

205220 E48007

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

```

Met His Ile Thr Leu Asn Ala Ile Leu Arg Ala Ile Phe Gly Ala Gly
 1           5           10           15
Gly Ser Glu Leu Asp Glu Leu Arg Arg Leu Ile Pro Pro Trp Val Thr
          20           25           30
Leu Gly Ser Arg Leu Ala Ala Leu Pro Lys Pro Lys Arg Asp Tyr Gly
          35           40           45
Arg Leu Ser Pro Trp Gly Arg Leu Ala Glu Trp Arg Arg Gln Tyr Asp
          50           55           60
Thr Val Ile Asp Glu Leu Ile Glu Ala Glu Arg Ala Asp Pro Asn Phe
65           70           75           80
Ala Asp Arg Thr Asp Val Leu Ala Leu Met Leu Arg Ser Thr Tyr Asp
          85           90           95
Asp Gly Ser Ile Met Ser Arg Lys Asp Ile Gly Asp Glu Leu Leu Thr
          100          105          110
Leu Leu Ala Ala Gly His Glu Thr Thr Ala Ala Thr Trp Ala Gly Arg
          115          120          125
Ser Asn Gly Ser Thr Gly Thr Pro Thr Cys Ser Arg Leu Trp
          130          135          140

```

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

```

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro
 1           5           10           15
Gly Tyr Pro Pro Thr Ile Glu Pro Ala Gln Pro Ala Val Ser Pro Pro
          20           25           30
Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro
          35           40           45
Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg
          50           55           60
Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp
65           70           75           80
Val His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala
          85           90           95
Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly
          100          105          110

```

205220" E4B4800T

Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val
 115 120 125
 Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala Arg Arg Ser Asp
 130 135 140
 Gly Lys Leu Val Leu Gly Ser Ala Asp Gly Ala Val Tyr Thr Leu Ala
 145 150 155 160
 Lys Asn Pro

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Trp Gly Ala Pro Pro Ser Gly Gly Pro Ser Pro Trp Ala Gln Thr Pro
 1 5 10 15
 Arg Lys Thr Asn Pro Trp Pro Leu Val Ala Gly Ala Ala Val Val
 20 25 30
 Leu Val Leu Val Leu Gly Ala Ile Gly Ile Trp Ile Ala Ile Arg Pro
 35 40 45
 Lys Pro Val Gln Pro Pro Gln Pro Val Ala Glu Glu Arg Leu Ser Ala
 50 55 60
 Leu Leu Leu Asn Ser Ser Glu Val Asn Ala Val Met Gly Ser Ser Ser
 65 70 75 80
 Met Gln Pro Gly Lys Pro Ile Thr Ser Met Asp Ser Ser Pro Val Thr
 85 90 95
 Val Ser Leu Pro Asp Cys Gln Gly Ala Leu Tyr Thr Ser Gln Asp Pro
 100 105 110
 Val Tyr Ala Gly Thr Gly Tyr Thr Ala Ile Asn Gly Leu Ile Ser Ser
 115 120 125
 Glu Pro Gly Asp Asn Tyr Glu His Trp Val Asn Gln Ala Val Val Ala
 130 135 140
 Phe Pro Thr Ala Asp Lys Ala Arg Ala Phe Val Gln Thr Ser Ala Asp
 145 150 155 160
 Lys Trp Lys Asn Cys Ala Gly Lys Thr Val Thr Val Thr Asn Lys Ala
 165 170 175
 Lys Thr Tyr Arg Trp Thr Phe Ala Asp Val Lys Gly Ser Pro Pro Thr
 180 185 190
 Ile Thr Val Ile Asp Thr Gln Glu Gly Ala Glu Gly Trp Glu Cys Gln
 195 200 205
 Arg Ala Met Ser Val Ala Asn Asn Val Val Val Asp Val Asn Ala Cys
 210 215 220
 Gly Tyr Gln Ile Thr Asn Gln Ala Gly Gln Ile Ala Ala Lys Ile Cys
 225 230 235 240

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

205220" E484800T

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

```

Asp Val Val Glu Ala Ala Ile Ala Arg Ala Glu Ala Val Asn Pro Ala
 1           5           10           15
Leu Asn Ala Leu Ala Tyr
                20

```

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```

Leu His Pro Ala Gly Ala Thr Asn Gly Ser Gly Gln Leu Ala Leu Pro
 1           5           10           15
Val Glu Ala Pro Pro Arg Ser Val Pro Ser His Gly Glu Pro Leu Gly
                20           25           30
Ser Ala Ala Pro Glu Gly Leu Glu Gly Glu Phe Asp Asp Arg Ile Asp
                35           40           45
Glu Arg Phe Pro Val Phe Ser Ser Ala Ser Leu Ala Glu Ala Leu Pro
                50           55           60
Gly Pro Leu Thr Pro Met Thr Leu Asp Val Gln Leu Ser Gly Leu Arg
                65           70           75           80
Ala Ala Gly Arg Ala Met Gly Arg Val Leu Ala Leu Gly Gly Val Val
                85           90           95
Ala Asp Glu Trp Glu Arg Arg Ala Ile Ala Val Phe Gly His Arg Pro
                100          105          110
Tyr Ile Gly Val Ser Ala Asn Ile Val Ala Ala Gln Leu Pro Gly
                115          120          125
Trp Asp Ala Gln Ala Val Thr Arg Arg Ala Leu Gly Glu Gln Pro Gln
                130          135          140
Val Thr Glu Leu Leu Pro Phe Gly Arg Pro Gln Leu Ala Gly Gly Pro
                145          150          155          160
Leu Gly Ser Val Ala Lys Val Val Val Thr Ala Arg Ser Leu
                165          170

```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

205220" 24848001

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```

Val Gly Val Val Gly Val Gly Ala Thr Ser Pro Ala Gly Ala Gly Ala
 1           5           10          15
Gly Ala Gly Ser Ala Gly Thr Gly Ala Gly Ala Gly Gly Gly Ala Thr
      20           25           30
Lys Gly Arg Ile Asp Ser Ala Ser Ala Leu Ala Ala Pro Leu Ser Thr
      35           40           45
Gly Leu Leu Ala Val Pro Ser His Thr Thr Asn Gln Arg
 50           55           60

```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```

Met Ala Asn Thr Gly Ser Leu Val Leu Leu Arg His Gly Glu Ser Asp
 1           5           10          15
Trp Asn Ala Leu Asn Leu Phe Thr Gly Trp Val Asp Val Gly Leu Thr
      20           25           30
Asp Lys Gly Gln Ala Glu Ala Val Arg Ser Gly Glu Leu Ile Ala Glu
      35           40           45
His Asp Leu Leu Pro Asp Val Leu Tyr Thr Ser Leu Leu Arg Arg Ala
      50           55           60
Ile Thr Thr Ala His Leu Ala Leu Asp Ser Ala Asp Arg Leu Trp Ile
      65           70           75           80
Pro Val Arg Arg Ser Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu
      85           90           95
Gln Gly Leu Asp Lys Ala Glu Thr Lys Ala Arg Tyr Gly Glu Glu Gln
      100          105          110
Phe Met Ala Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Pro Ile Glu
      115          120          125
Arg Gly Ser Gln Phe
      130

```

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

```

Pro Gly Ser Phe Ala Arg Thr Lys Pro Pro Gly Arg Thr Ala Asp Ala
 1           5           10           15
Pro Ile Arg Cys Arg Asp Ser Arg Gly Thr Ala Gly His Arg Ala Leu
          20           25           30
Asp Glu Pro Pro Pro Arg Gly Ser Glu Pro Ala Arg Arg Arg Ser Arg
      35           40           45
Gly Val Arg Thr Val Val His Asp Ser Leu Ala Ala Arg Arg Val
 50           55           60

```

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

```

Gly His Gly Gly Gln Ser Ala Ile Gly Leu Gly Gly Gly Ala Gly Gly
 1           5           10           15
Asp Gly Gly Gln Gly Gly Ala Gly Arg Gly Leu Trp Gly Thr Gly Gly
          20           25           30
Ala Gly Gly His Gly Gly Ala Arg Arg Trp Tyr Arg Gly Pro Thr Ala
      35           40           45
Ala Arg Ser Gly Arg His Gly Arg Arg Gly Trp Arg Arg Trp Ala Asp
 50           55           60
Arg Gln Arg Arg Gly Arg Arg Arg
 65           70

```

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

```

Asp His Arg Arg Arg Ser Leu Ala Ser Leu Arg Ser Ala Ser Ser Pro
 1           5           10           15
Ala Arg Ile Thr Glu Val Arg Pro Cys Thr Pro Leu Leu Glu Arg Ser
          20           25           30
Ala Pro Gln Ser Gly Ser Arg Asp Pro Phe Arg Pro Trp Pro Ala Asp
      35           40           45
Ala Gly His Ala Arg Ser Pro Ala Trp Tyr Arg Leu Gly Ala Gly Asn
 50           55           60

```

Pro Ile Pro Val Arg Ala Ala His His Glu
65 70

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCGCACGTAA | CACCGTGAAT | TGAAGGGAGC | CGCTGGTCAT | GGGCCGATTC | TATCCGTGGG | 60 |
| CGAACGGTTA | TTGACGGCCC | GGAGGCCACT | CCGCTGCCAC | CAAGTGGTGA | CTCAGCGCGT | 120 |
| TTTCACGGCA | ACGAACGGCG | GACACACCAC | TTGACATTCG | ACAGCACGGC | CGCG | 174 |

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TCGCAAACGG | GGTGACGTTT | CGTCCGGTGG | CGCTAGAGAG | TTTGTCGCAC | TTTCCGGTGA | 60 |
| CCGTCGCCGC | GCACCGCAGC | ACCGGTGAGC | TCACGCTGCT | AGTGGAGGTG | CTCGACGGTG | 120 |
| CGCTGGGCAC | GATGGCGCCC | GAAAGCCTCG | GCAGGCGGGT | GCTGGCTGTG | TTACAGCGCT | 180 |
| TGGTCAGCCG | GTGGGATCGG | CCGCTGCGCG | ACGTCGACAT | TCTGCTGGAC | GGCGAGCACG | 240 |
| ATCCGACCGC | ACCCGGCCTG | CCGATGTGA | CGACGTCGGC | ACCCGCGGTG | CATACCCGGT | 300 |
| TCGCCGAAAT | CGCTGCGGCA | CAGCCTGACT | CGGTGGCGGT | CAGTTGGGCG | GATGGTCAGC | 360 |
| TGACGTACCG | GGAGCTGGAT | GCATTGGCCG | ACCGGCTGGC | CACT | | 404 |

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Asn | Gly | Val | Thr | Phe | Arg | Pro | Val | Ala | Leu | Glu | Ser | Leu | Ser | His |
| 1 | | | | | 5 | | | | 10 | | | | | 15 | |
| Phe | Pro | Val | Thr | Val | Ala | Ala | His | Arg | Ser | Thr | Gly | Glu | Leu | Thr | Leu |
| | | 20 | | | | | 25 | | | | | | 30 | | |

205220" E484800T

Leu Val Glu Val Leu Asp Gly Ala Leu Gly Thr Met Ala Pro Glu Ser
 35 40 45
 Leu Gly Arg Arg Val Leu Ala Val Leu Gln Arg Leu Val Ser Arg Trp
 50 55 60
 Asp Arg Pro Leu Arg Asp Val Asp Ile Leu Leu Asp Gly Glu His Asp
 65 70 75 80
 Pro Thr Ala Pro Gly Leu Pro Asp Val Thr Thr Ser Ala Pro Ala Val
 85 90 95
 His Thr Arg Phe Ala Glu Ile Ala Ala Gln Pro Asp Ser Val Ala
 100 105 110
 Val Ser Trp Ala Asp Gly Gln Leu Thr Tyr Arg Glu Leu Asp Ala Leu
 115 120 125
 Ala Asp Arg Leu Ala Thr
 130

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCTTCGACGG | CTACGAGTAC | CTGTTCTGGG | TGGGTTGTGC | GGGCGCCTAC | GACGACAAGG | 60 |
| CCAAGAAGAC | CACCAAGGCC | GTCGCCGAGC | TGTTCCGCGT | CGCCGGGGTG | AAATACTTGG | 120 |
| TGCTGGGCGC | TGGGGAAACC | TGCAACGGCG | ACTCGGCGCG | CCGCTCCGGC | AACGAGTTCC | 180 |
| TCTTCCAGCA | GCTGGCACAA | CAGGCCGTCG | AGACCCTGGA | CGGTTTGTTC | GAGGGTGTGG | 240 |
| AGACCGTCGA | CCGCAAGATC | GTTGTCACCT | GCCCGCACTG | CTTCAACACC | ATCGGCAAGG | 300 |
| AATATCGGCA | GCTGGGCGCC | AACTACACCG | TGCTGCACCA | CACCCAGCTG | CTCAATCGGT | 360 |
| TGGTGCGCGA | CAAGAGGCTG | GTCCCTGTCA | CTCCGGTTTC | TCAGGACATC | ACCTACCACG | 420 |
| ACCCGTGCTA | CCTGGGTCCG | CACAACAAGG | TCTACGAGGC | ACCACGGGAG | CTGATCGGTG | 480 |
| CCGCGGGGGC | CACCTGAGCC | GAGATGCCGC | GCCATGCCGA | CCGCAG | | 526 |

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| CTCGCCGCCG | TGATCTGGCC | GGCGAACTTC | GTCAGTGCAT | CCAGACCCCA | ACGATCATCG | 60 |
| ATCAGGCCGA | TGCCCCATGAT | CACCGCACCG | GCCACCAGCA | CCGCGGGCAT | GCCGGTGGAA | 120 |
| TAGACGAACC | CCCGGGTGAG | TGCCGGAAGC | TGGGAGGCAA | GAAAGACGGC | GCCGACAATG | 180 |
| CCCAGGAACA | TCGCCAACCC | ACCCATCCGA | GGGGTAGGCG | TGACGTGCAC | ATCTCGCTCC | 240 |
| CGCGGGTAGG | CGACGGCTCC | CAGGCGACTG | GCCAGCATCC | GCACCGGACC | GGTCGCAAAA | 300 |
| TAGGTGATGA | TCGCCGCGGT | CAGCCCCACC | AGCGCAAGCT | CACGCAGCGG | GACACCGGCG | 360 |

| | |
|---|-----|
| CCGCGATAGG ACAGGGCGAG CAAGCCACCG GCAACGCCGG CCACATCGCT GGACACCTCG | 420 |
| AGACCGTACT GCACCAACCT GAAGAGCTGA ACACTCGCCG AACGTGCAAC AGCTGCGAAC | 480 |
| AATTGGG | 487 |

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

| | |
|---|-----|
| ACGAAGCGCG AGAATATGAG CCGGGGCAAC CCGGCATGTA CGAGCTTGAG TTCCCGGCGC | 60 |
| CTCAGCTGTC GTCGTCCGAC GGCCGTGGTC CGGTGTTGGT GCACGCTTTG GAAGGTTTCT | 120 |
| CCGACGCCGG CCATGCGATC CGGCTGGCCG CCGCCCACCT CAAGGCGGCC CTGGACACAG | 180 |
| AGCTGGTCGC GTCCTTCGCG ATCGATGAAC TACTGGACTA CCGCTCGCGG CGGCCATTAA | 240 |
| TGACTTTCAA GACCGATCAT TTCACCCACT CCGATGATCC TGAGCTAAGC CTGTATGCGC | 300 |
| TGCGCGACAG CATCGGCACC CCATTTCTGC TGCTGGCGGG TTTGGAGCCG GACCTGAAGT | 360 |
| GGGAGCGGTT CATCACCGCC GTCCGATTGC TGGCCGAGCG CCTGGGTGTA CGGCAGAACC | 420 |
| ATCGGCCTGG GCACCGTCCC GATGGCCGTT CCGCACACAC GACCGATCAC GATGACCGCT | 480 |
| CATTCCAACA ACCGGGAGCT ATCTCCGATT TTCAACCGTT CGATCTCC | 528 |

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

| | |
|---|-----|
| CCAAGCCCGT CAAGGAGCCG GTGCCGGCCT TGCTCCGGT GCCGCCGACG CCGGCGTTGC | 60 |
| CGCCGTTGCC GCCGTTGCCG CCGGTACCGG GGTTCCTAC GGTGCCGCCG CCCGGCAGCA | 120 |
| TGGCCCCGCT GTTTAGGCCG TTTTCGCCG CCCC GCCGTC ACCGGCTTTG CCGCCATCGC | 180 |
| CGCCGTTGCC GCCGCTGGTG GGGGTGGCGG CCTGTTGAC GTATTGTTCC ACCGGCCCCG | 240 |
| CCCTTGACCC TTTGGCGGTG TCGATCGCGG CGTCGATGGA TCCGCCGACC ACGAGTGCG | 300 |
| AAGCCTCGCC TGCCGCCGCA GCCGCCAAC TGTGTCGCGG CTCCTGCGAT TTGGCCCCCG | 360 |
| CCGACGAGAT GATGGGCACC ACCGGAGCCT GCGGCCGTCT GGGGGAGGCC AGCGCGGGTT | 420 |
| CGCGGTCACG CCATACGCGA CGGTGCGCCG CCGCTTCGGA GATTTGCAGG CTGCGTTGCA | 480 |
| CCAGATCGAG CAGCGGTGTG CCCAGGGACT GGGTTAGCCC GTTGGCGCCG CCGTTGTAGC | 540 |
| GGCGAGCGCA ATATCGGTGC CCACTCGACC CAACCGCGAC TCCATAAGCG ACACCATTGC | 600 |
| CGGTTGATGC | 610 |

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

```

Phe Asp Gly Tyr Glu Tyr Leu Phe Trp Val Gly Cys Ala Gly Ala Tyr
 1           5           10           15
Asp Asp Lys Ala Lys Lys Thr Thr Lys Ala Val Ala Glu Leu Phe Ala
      20           25           30
Val Ala Gly Val Lys Tyr Leu Val Leu Gly Ala Gly Glu Thr Cys Asn
      35           40           45
Gly Asp Ser Ala Arg Arg Ser Gly Asn Glu Phe Leu Phe Gln Gln Leu
      50           55           60
Ala Gln Gln Ala Val Glu Thr Leu Asp Gly Leu Phe Glu Gly Val Glu
65           70           75           80
Thr Val Asp Arg Lys Ile Val Val Thr Cys Pro His Cys Phe Asn Thr
      85           90           95
Ile Gly Lys Glu Tyr Arg Gln Leu Gly Ala Asn Tyr Thr Val Leu His
      100          105          110
His Thr Gln Leu Leu Asn Arg Leu Val Arg Asp Lys Arg Leu Val Pro
      115          120          125
Val Thr Pro Val Ser Gln Asp Ile Thr Tyr His Asp Pro Cys Tyr Leu
      130          135          140
Gly Arg His Asn Lys Val Tyr Glu Ala Pro Arg Glu Leu Ile Gly Ala
145          150          155          160
Ala Gly Ala Thr

```

(2) INFORMATION FOR SEQ ID NO:300:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 161 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

```

Arg Arg Arg Asp Leu Ala Gly Glu Leu Arg Gln Cys Ile Gln Thr Pro
 1           5           10           15
Thr Ile Ile Asp Gln Ala Asp Ala His Asp His Arg Thr Gly His Gln
      20           25           30
His Arg Gly His Ala Gly Gly Ile Asp Glu Pro Pro Gly Glu Cys Arg
      35           40           45
Lys Leu Gly Gly Lys Lys Asp Gly Ala Asp Asn Ala Gln Glu His Arg
      50           55           60
Gln Pro Thr His Pro Arg Gly Arg Arg Asp Val His Ile Ser Leu Pro
65           70           75           80
Arg Val Gly Asp Gly Ser Gln Ala Thr Gly Gln His Pro His Arg Thr
      85           90           95
Gly Arg Lys Ile Gly Asp Asp Arg Arg Gly Gln Pro Asp Gln Arg Lys

```

205220 E4843001

[illegible]

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

| | | | | | | | | | | | | | | | |
|------------|-----|-----|-----|----------|-----|-----|-----|-----|-----------|------------|-----|-----|-----|-----|------------|
| Glu 1 | Ala | Arg | Glu | Tyr 5 | Glu | Pro | Gly | Gln | Pro 10 | Gly | Met | Tyr | Glu | Leu | Glu |
| Phe | Pro | Ala | Pro | Gln | Leu | Ser | Ser | Ser | Asp 25 | Gly | Arg | Gly | Pro | Val | Leu |
| Val | His | Ala | Leu | Glu | Gly | Phe | Ser | Asp | Ala | Gly | His | Ala | Ile | Arg | Leu |
| Ala | Ala | Ala | His | Leu | Lys | Ala | Ala | Leu | Asp | Thr | Glu | Leu | Val | Ala | Ser |
| Phe 65 | Ala | Ile | Asp | Glu | Leu | Leu | Asp | Tyr | Arg | Ser | Arg | Arg | Pro | Leu | Met 80 |
| Thr | Phe | Lys | Thr | Asp | His | Phe | Thr | His | Ser 90 | Asp | Asp | Pro | Glu | Leu | Ser |
| Leu | Tyr | Ala | Leu | Arg | Asp | Ser | Ile | Gly | Thr | Pro | Phe | Leu | Leu | Leu | Ala |
| Gly | Leu | Glu | Pro | Asp | Leu | Lys | Trp | Glu | Arg | Phe | Ile | Thr | Ala | Val | Arg |
| Leu | Leu | Ala | Glu | Arg | Leu | Gly | Val | Arg | Gln | Asn | His | Arg | Pro | Gly | His |
| Arg 145 | Pro | Asp | Gly | Arg | Ser | Ala | His | Thr | Thr | Asp 155 | His | Asp | Asp | Arg | Ser 160 |
| Phe | Gln | Gln | Pro | Gly | Ala | Ile | Ser | Asp | Phe | Gln | Pro | Phe | Asp | Leu | |

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

Lys Pro Val Lys Glu Pro Val Pro Ala Leu Pro Pro Val Pro Pro Thr
 1 5 10 15
 Pro Ala Leu Pro Pro Leu Pro Pro Leu Pro Pro Val Pro Gly Phe Pro
 20 25 30
 Thr Val Pro Pro Pro Gly Ser Met Ala Pro Leu Phe Arg Pro Phe Ser
 35 40 45
 Pro Ala Pro Pro Ser Pro Ala Leu Pro Pro Ser Pro Pro Leu Pro Pro
 50 55 60
 Leu Val Gly Val Ala Ala Trp Leu Thr Tyr Cys Ser Thr Gly Pro Ala
 65 70 75 80
 Leu Asp Pro Leu Ala Val Ser Ile Ala Ala Ser Met Asp Pro Pro Thr
 85 90 95
 Thr Thr Cys Glu Ala Ser Pro Ala Ala Ala Ala Gln Leu Cys Arg
 100 105 110
 Gly Ser Cys Asp Leu Ala Pro Ala Asp Glu Met Met Gly Thr Thr Gly
 115 120 125
 Ala Cys Gly Arg Leu Gly Glu Ala Ser Ala Gly Ser Arg Ser Arg His
 130 135 140
 Thr Arg Arg Cys Ala Ala Ser Glu Ile Cys Arg Leu Arg Cys Thr
 145 150 155 160
 Arg Ser Ser Ser Gly Val Pro Arg Asp Trp Val Ser Pro Leu Ala Pro
 165 170 175
 Pro Leu

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

AATTCGGCAC GARCAGCACC AACACCGGCT TCTTCAACTC CGGCGACGTC AATACCGGTA 60
 TCGGCAACAC CGGCAGCTTC AACACCGGCA GCTTCAATCC GGGCGATTCC AACACCGGGG 120
 ATTTCAACCC ANGCAGCTAC CACACGGGGA CTCGGAACA CCGGCGATTT TACACCGGCS 180
 CCTTCATCTC CGGCAGCTAC AGCAACGGGT CTTGTGGAGT GGAAATTATC AGGGCTCATT 240
 GGNTGCACCC GGSCTTRCGA ATCCCTCGKG CCAATTCAAC TCCTCNACAA GCTTGC GGCC 300
 GCACTCSAGC CCGGGTGAAT GATTGAGTTT AACCGCTNAN CAATAACTAG CATAACCCCT 360
 TKGGGCCTCT AAACGGGTCT TGAAGGGTTT TTTGCTGAAA GGANGAACTA TATCCGGATA 420
 ACTGGCGTAN TACGAAAAGC CGCACCGATC GCCTTCCCAA CAGTTGCGCA CCKGAATGGC 480
 AATGGACCNC CCTKTTACCG GSCATTAACN CGGGGGTGTN GGKGTACCC CCACGTNACC 540
 GCTACCTTGC CANNSSCTN RSGCCGTCTT TCSTTTCTTC CTTCTTCTC CCMCTTCGCC 600
 GGTTCCCNCT AGCTCTAAAT CGGGGNNCCC TTTMGGGTTT CAATTATTGC TTACNGSCCC 660
 CCACCCCAAA AAYTNATTNG GGTTAATGTC CCTTMTTGGG CNTCCCCCTA WTNANNGTTT 720
 TCCCCCTTNA CTTTGRSTCC CTTCTTTATW NTGAMNCTNT TTCCACYGGA AAAMNCTCCA 780
 CCNTTYSSGS TTTCTTTTGA WTTATMRGGR AATTSCAATY CCGCYTTKGG TTMAANTTAA 840
 CYTATTTTCA ATTTTCCCGM TTTTMMNATR TTNSNCKCGM KNCTCCNRKA SSGNTTTCCT 900
 CCCCCYTTSS GKTYCCCCRN G 921

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| AATTCGGCAC | GAGATANGGG | CGCACCGGGG | TCCGCAGCCG | GCGGGACCGT | CGCCAGCACC | 60 |
| ACCGGGGTCA | ACAGCACCAC | GGTGGCGTCC | ANGCAGAGCG | CCGCGGTGAT | GGCGGCCGAG | 120 |
| ACGGCRAACA | CCTGCCGTAG | CAGTCGGTGC | GACTCCGCGC | TCGCTCGANC | CATGGCCGCG | 180 |
| CCGGCTGCCT | CGAACANGCC | TTCGTCTGTC | ACAGCTTAGC | CAGCANCCAA | ACCGCACCCA | 240 |
| GAAACCCACA | CGCCCGCCGC | CCCGGANACC | TGCGCCATCG | KCTGCTGGGG | CGANATCCCC | 300 |
| CGATCGCTNA | CANGATGACC | GCTGCCGGAA | CGCCGCCGCT | GCCTCCGGGC | AGCCGCGTGG | 360 |
| GCSGGGCAAC | CGCGAACCCA | NGAACACGGC | AAGCAGTATC | ANCGCAACAG | CAATTGTCAA | 420 |
| GGGCTAAACG | CTTCACATCC | AGGGATCTCG | CGGCGCCACA | CCGTCCGMTC | TGCAGSGCGA | 480 |
| CCCCNTCCTN | GGGCGGNCAC | TCNTCAAAGA | TGCNGATCNA | CAGKCTAGGT | CTTCGGCCGA | 540 |
| TATGSAAGGN | CCCAACGGNT | TTAAAGCGGC | SAAAAAATC | TCCCANTGGA | TAAAATCAGC | 600 |
| CGGGGANCCC | CCCGTGSCMM | NGTCYCGGKC | ATTNTTCAAC | MGGTTTNACG | GCGGKTGCNG | 660 |
| GCCAACKTGC | CAAAMTTAAG | KTNNGGGNTY | CGGGGCGGTA | ACCGGCNNTK | NGCCCCTTAA | 720 |
| AAAACCGGNC | YTTTCTKGAT | TAMMACCGGN | CCCCCAWTGG | CGGKTGKTCC | CANGNTYAAC | 780 |
| AMCCYCCCCS | MNGGGKTGGS | SAACCCTTCC | CGNGGGGTTC | NTKGTTSCYT | AWMCCCCCGG | 840 |
| AAACCSGKYG | GGKTGGCRTN | WASSAMNCCC | CMNGYYTCTT | TAAAGGCCAN | KNRAAWGKYT | 900 |
| CCTTGGAAW | CCTNCAATYC | GAAAAYYCTC | CTYMMGSSCN | CTTKCWRTYN | NRNGGGAACS | 960 |
| AMWTNYCCNC | GWTTCAWTCG | GGTCCGASMN | AAACKCTTTY | TTTTYCGSSC | STCCMGSNC | 1020 |
| SGGTKNANAN | AAASATTTMC | YYCNNNANKK | YYCSSGCTT | CYKMGRNRNR | GMGAACCCGR | 1080 |
| GS | | | | | | 1082 |

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| AATTGGCACG | AGTGATCGCG | CTGAAGCCGG | TAGCGCGGGT | GGCTCGGGTG | GTTTGCGAAC | 60 |
| RAAATCCGCT | CGANGTGGTC | TCGGTAGGCG | GTGTCCANAA | CGGTGGCGCG | GTGCCGGCGG | 120 |
| ATCTGATCGG | CGCGGCCGTA | GTGCACGTGC | GCGGGCGTGT | GCAGTCCGAT | GCCGGAATGC | 180 |
| TTGTGTTCTG | GGTTGTACCA | GCCGAAGAAC | CGGTGCGAGT | GCACCCGGGC | CGCCTCGATC | 240 |
| GACTCGAACC | GTTTCGGGAA | ATCGGGCCGG | TACTTGAAGG | TCTYGAAGTG | GGCCTCAGAC | 300 |
| AACGGGTTGT | CTTGCTGGTG | TGCGGGCGTG | AGTGCGACTT | GGTGACACCG | AAGTCGGCCA | 360 |
| NCANCAATGC | CACCGGTTTG | GAATCATCC | ACAACCCCCG | TCCGCGTCMA | GGTCACTTGT | 420 |
| NCGGCGCTAA | TTTNYTGGGC | GGCAAGGGTT | TGCCGAYCAN | KCCGCTCGGC | CAAAACTTCG | 480 |
| ANTCNCSCCA | AGGCCNCCAT | CCNCCCAAAC | AMGTTACGGG | ANAAAAANATY | CAAAGAYCAC | 540 |
| CYTCCGGKTN | TTATANCTYC | CCYTTTGSTY | GGGCCCCCN | CYYTGKKNAT | ACCCCTNCCA | 600 |

| | | | | | | | | |
|------------|------------|-------------|------------|------------|------------|------------|------------|-----|
| AWTCCCAACN | CCCKCCAANA | RCYKGGGGCC | CCCNCCAACC | CGGGKGAACA | WTAATTTAAA | 660 | | |
| CCCYAACMAW | ACTWMMNACC | CNNGGGSCCY | AAMCGTYYNR | AGGTTTTSCT | NAAAGAAASA | 720 | | |
| ANTCGGAAMC | CGGNTSTACC | AAAAASCCCK | CCNWTCCCTC | CRASATTGSC | NCCSAAWKSA | 780 | | |
| AKGCCCCCN | Y | TCSGCNWN | NC | CSGCGGKKKT | KKGTTNCCCT | WMRCWMWYTS | GGCCNASCCN | 840 |
| CKYYSSMYCC | CCCC | TCCCCM | CTCCGNKTCC | CCAMCCYANC | MGGCCCCYTM | GKKCCCWKNT | 900 | |
| YKGGCCCCC | AMMNNNGGG | WGACCCTNGG | CCCCMKRRGM | TCCCNANTGA | MCCTCWGNRA | 960 | | |
| MKCYCCNRAR | ANMCCSCNCC | NGCNCRCCKNN | | | | 990 | | |

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

| | | | | | | |
|------------|------------|-------------|------------|-------------|------------|-----|
| AATTCGGGTG | GCAACGCGGG | CCTGTTTCGGC | AACGGCGGCG | CCGGTGGTGC | CGGTGGGGCT | 60 |
| GGTGGTGGCG | CCGGCGGCGC | GGGCGGTAAC | GCGGGGTGGT | TTGGTCATGG | GGGCGCTGGC | 120 |
| GGCGTGGGTG | GTGTANGTGC | GGCCGGGGCC | AACGGTGCTA | CGCCCCGGTCA | GGATGGGGCG | 180 |
| GCTGGTGTG | CCGGGTCGGA | CRACRCTCGT | GCCGCTCGTG | CCG | | 223 |

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| AATTCGGCAC | GANGCGGCAA | CGGTGGCAGC | GGCGGCACGT | CNGTTGCCAC | CGGGGGGGCC | 60 |
| GGGAACGGCG | GTGCCGGCGG | CGCCGGCGGC | GGGGCCGGGC | TGATCGGCAA | CGGCSGCAAC | 120 |
| GGCGGCAGTG | GCGGAATGGG | CGATGCCCCG | GGCGGCACCG | GCGTCNGCGG | CATCRGTGGG | 180 |
| CTGTTGTTGG | GTTTGGACRG | CGCCAACGCC | CCGGCCAGCA | CCAACCCGCT | GCACACCGCG | 240 |
| CAGCACAGGC | GTTGGCCGCA | GTCAACGCGC | CCATCCAGGC | CGTGACCGGG | CGCCCCCTGAT | 300 |
| CGGCAACGCG | CCAACGGCGC | CCCGGGCAAC | GGGGCCCCCG | GCRGGCACGG | CGGGTGGTTG | 360 |
| TTCGGCGGCG | GAAGGAACGG | CGGGTCCGGC | GTCANCRGCG | GGGCGGGCGG | AAATGCCG | 418 |

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| AATTCGGCAC | GAGGGGCACG | ATCGCATACA | GCGCTCGCGG | CAGACCCGCC | CGATACAGCA | 60 |
| GCTCGGCACA | CGCGAGCGCA | CAATACGGCG | TCTGGCTGTC | CGGCTTGARC | ACCACCGCGT | 120 |
| TACCGGCCAC | CAGCGCGGGC | ACCGAGTCCG | ACACCGTAAG | CGTCATGGGG | TAGTTCCACG | 180 |
| GCGAGATCAC | CCCCACCACG | CCCTTCGGTT | GATAGCACAC | CGTGGTCTTG | CCTATCCCGG | 240 |
| GCAGCAGCGG | CTGTGCCTTA | CGGGGCTTCA | GCAGGTCCAC | ACAGACTCGT | GCSTTATAAT | 300 |
| TNCGCSTTCC | GCGATCAGAT | CGACAATTTT | CTCTTGCGCC | GCCCATCGGG | CCTTGCCCGC | 360 |
| CTCGGCTTGC | AGGAAGTCCA | TGAAGAACTC | GCGGTTCTCG | ATNAACAGGT | CGCGATAGCG | 420 |
| GCSGATGACT | GCAGCTCGCT | CGATNACGGG | ACCTTCGCCA | GTCGGTCTGC | GCCGCGCGAN | 480 |
| CTTCCGCGAA | TGCCGCTTCG | ACTTCCGCGG | NCGTGCCAAC | GGAATCNTAT | CACGGGTTGC | 540 |
| CGGTAAAAAC | TCCTCAATST | NCYGGTCGAA | ATTCCGCAAC | TTCTTATCCC | GGCAGGTRCC | 600 |
| AACSANNCAA | ACCTCGGCAA | GGTTAGGTTT | TCCCCNCTT | YCAAAAATNC | GGKTTTTGGN | 660 |
| CMAATTTTCG | CKCNATGKTG | MCAAGGMTCT | CKAANAAKCS | GGGTCYTCTN | NTCNGKGGAK | 720 |
| CCAAAMGGKT | TTGGGGMAGC | GKNMNCCAA | CCTWACCCTG | KTKAANGGNW | TTCCCCCGG | 780 |
| GGGAKKNGA | ATYCYCCSNA | NCCCRGGGGG | GNMCAARATC | TYCCGGMCTC | CTCKGGAWTC | 840 |
| WGMGSTTTCC | CAAAAAACSC | CCCAAATMM | TTTTTCCRCN | TRTTGANACW | CTTTTKARCA | 900 |
| MMCSSAARNS | ANMCNCTCYC | CKCTKTGKTK | AAAAAGNAYW | CCCCMAAATT | TYTAWTTSSC | 960 |
| CCSCGCGGGN | CCCNCTNTTT | TSCNMTWCTM | WNYTNCRMCC | MMMSNCKSNG | KKGGNRCCNN | 1020 |
| CRCCSNCCCM | AAWYNTKGYN | KNTATMAGC | | | | 1049 |

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|------|
| AATTCGGCAC | GAGGGAATCG | AGAATCCCGG | AATGGTGAAG | CCTCGGTGCC | TGCCGTTACG | 60 |
| CCAAGAKTCA | GGGTGAGCGG | CCCCCCGGTG | GGAATGCTGA | SGCCAACCGG | GAAAAGGGTG | 120 |
| AGGGCTGGGG | TGGAATAACT | GAANGTTACT | GGGATGGAAA | ACCCGGTATT | GATATGTATT | 180 |
| GGGCCGATCA | ANGTTGTGGG | AATGGGGGAA | GGCTGAGGGC | GACCTGTTGG | ATTTGGGGAA | 240 |
| TTGTYRTGGA | CRAKACWGGC | CAGCCMGCGT | GATGGTTTGG | T TSAANTTTT | GTGCCGSCCA | 300 |
| CANGGTGATG | GGATTGATTT | TGATGGGGCC | SATCGAAATA | TTGGGTATGC | CNACGCCSAA | 360 |
| CGAGATYGCC | GGGACGTTCA | TGGGCGGGAC | AACCMASGGT | CCSANGTAAK | GGTTTCCTTN | 420 |
| ATNTTGATCG | GGATTCCGGA | ACTMTSTCGA | TGSGCTCSAY | MTSATSGCCC | NACNCCWCCG | 480 |
| YTTATTTTMS | GCTNAYGGGA | ATBAMRGGA | CAAYNTCCCT | CCCMGGAAAA | ACCAACMSGC | 540 |
| CCTGGTNSYC | CNCCCRCCNC | AKAACCRTT | KCTGTRSTMC | CCSMAAATNA | CSCCSCCTTS | 600 |
| NACTCCNCSG | AANTNSCCCC | CCSCCKNNTT | ATSTYCCCGK | GTTCCCCCMC | CCCTTNAAMC | 660 |
| TCCCCGGTTA | ACCCCCWTNT | SNCNCCCCCS | YTAAMNCRG | GCTTSTTNCT | CCCCCYTRMK | 720 |
| CNCCCCCTCK | SAMCWNCNC | CTCKAACNAC | CCCKCYKGS | TNCCCAATNT | WCMWCKCCNS | 780 |
| KTTNTMCTKC | CCAAYTNCRC | CCNCRCTCCC | CKKSTSTCAM | WTATAAAACC | WCWYAWYNNK | 840 |
| KCNCWMAWTA | MGACWCTCNY | NCCCCNCNCK | NTTKTAMWCC | CKMCCCKCSW | TWCYCKCSCC | 900 |
| CCMTCTMNAC | YCCCCCKKTY | NKWMCCCTTC | CCCCCCTCCC | MCNMBMKTCT | YCSGKTWCWC | 960 |
| NCYNTTMTCN | CYNANMCKCK | KTCTCTTCN | CRNTCTCCCC | CCWCCCCCV | KKCTCTSKCC | 1020 |
| CNCNCTCCSC | MMKGSC | | | | | 1036 |

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

| | | | | | | |
|-------------|-------------|------------|------------|-------------|-------------|------|
| AATTCGGCAC | GAGATCATGA | ATAGCGGGCT | GGTCAGCACC | GAAGTGGTCG | GCGATCTCGC | 60 |
| GAGCAAGTCT | CGTCTGCTCG | CCCAGCAGGA | GGTCGGCATC | GATGCGGACA | CCTGCGATGT | 120 |
| CTTGGATGGT | GTTCAGTTGC | AGGTAAGGCC | GACGCCGCAG | CTTTGCTAGC | AGGGTGTCTT | 180 |
| GGCTCTTCGC | ACGTGAGGTA | ACCAATAACT | CCGACGCAGA | CCAAC'TCCGG | CCCTCGATCC | 240 |
| GGGTACCAGG | CTCCGCCGGA | GCCAGCCGTT | GTGCCCCCTG | GGCCGAAGGT | CAGCTGCTGT | 300 |
| GCGATCGAAG | TAAGAAACCG | CGCCATGCCC | GTGCGCAAGT | ACGACTGACC | GAGCAAACGA | 360 |
| ACGATCGTCG | TCCTTTCCGT | GGGGGTAATC | GANCCCAGCA | ACCGCACGAG | CCACCAATCA | 420 |
| TTGGGATTTCG | GCCACTGACC | GACCAACCGC | CTGTGCGACA | CCCCAGCGGA | ATTGGTGGTC | 480 |
| TTCCGCGGGG | CCGCNAACGG | AATCANCGSG | ACGCGCTCGC | CGAASCANCC | GCATANCCNT | 540 |
| ACATANCAAC | GGNNTCTGCG | CCCACATTTT | GGGSTTMTGC | CCCTCNGCAA | CSSNAAYNCC | 600 |
| CCCAATTCYG | AACNAAAAAA | TTGGYCCATY | ARNGTYCTCM | CCAAAAACCN | AWTCCCCCKTA | 660 |
| TCCCCCGGGG | GGGRCCCCYY | NMNAAAACGG | CCCWAAANCC | CCSGGGCSCC | CGGGTTRWTN | 720 |
| CCCCTTGTGC | GCCCNCCSGG | TTTGGTCMCM | GGSCMTNWN | GGGNTGCSCC | CCNCNAAAA | 780 |
| AAAAAYCKNG | NCAAAATYAAA | CCCKYCMAAA | ASKTGGGSSC | CCCMARCCGG | GGKAAKKWWA | 840 |
| ANTTAANCCN | KAAAAAAAWW | NCANNMCCCC | NGGGNCCTAA | GGKYTTAGGG | GTTSTTNANG | 900 |
| ARAAAATMTC | CANATMNSSK | TTNNAAAAAA | ASCCSWAKCC | CCCNNNKKNN | CCAAWKAARR | 960 |
| SRCCTTCGGG | TNWNSSGGGG | KKKKKNTCMS | KMNMTTWGR | CCCNCCGCCN | NNTWKCTTN | 1020 |
| TCCNYGGNGC | RNCAGN | | | | | 1036 |

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1060 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|-----|
| AATTCGGCAC | GAGTCGATTC | GATCGAACAC | GCCCCGACCT | GGCCAGGCCA | CATGGGCGCG | 60 |
| GCCATGGCCA | ACGCCTACTC | GGCCAACCCG | AATCCATTCG | GCGTCTCACC | GCAACCCCCG | 120 |
| AAACCGGCGA | CCGCGGCATG | GATCAACCCG | CCCACCCCAG | ATCCGAAATA | GCGTCCACAT | 180 |
| AATGAGACAC | TGGCGCAAAG | AGCTTGACAG | GCGCCGCACC | ACGCAAGCTG | TTAGACGTGT | 240 |
| CGGTCTTGCA | AGAAGCGGGT | TGGCCACCCA | AGATCACGCC | GCCCAAGGGC | ATCGAGTCAA | 300 |
| CGTTGCGGTG | GTATCGCGCT | AACGTCGGCG | CCGCCAAGAA | ATGACGGTGC | GCATTACCAT | 360 |
| GGCCCTGCTG | ATCACCTTTG | GCCACCTGCG | CACCANAACT | ATGANACGCC | TTATGCCGAG | 420 |
| TCTCGTGGAC | ATCGGCAGCC | GCTTCAAAAA | CTCCTTGTCG | ACAATSGTAT | TGCTGANCCG | 480 |
| CCGAATCTTT | NTRCTTGCAA | SAACACTNCA | TGTTCNSGGT | NAACAACCYT | GGTTNGAAAA | 540 |
| ACANAACATA | TTGAANTCCC | ANTCGGGCAM | GAACCNGTMT | CGGAAGKTGK | TGGGAACGAA | 600 |
| TGKTGCCCAA | AAATCCCGGG | NGGTRAAAWW | CCCNNSNATGG | MSAATTTTSC | CTNGAACAAAM | 660 |
| AAAAGGTCCA | AGKYCAAAGG | NGCCCCCCCC | SGNAAATTGG | TGAACSCAKA | WYANRTTCCC | 720 |
| WWWTNCAAT | MTTNGGGTCC | KNNTCCCCWT | AAANGGGSCN | CCCCNCCRG | GMGTYTCCCC | 780 |
| NWNMGGMGN | CYYCSCCCCA | AAAAAAAMMM | MTTTCSGKGG | SMGGKKCCCC | CCSGGTYWGG | 840 |
| GKKYTAAAC | CCGGKGGGTN | CAAAAAANAN | ACCCCCCAMS | NGGGGGGAAA | ATTTGNAAWT | 900 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| AAGGKKKTKC | SCMACCCCAA | AAANMMNNCN | AWNCCCGMGK | SARGGGGRNY | TTMKAGGGMG | 960 |
| GNYYYYCCW | YCGGGGGGNA | NAAYAAAAGK | NGSNGRGAAT | NTTNTTTTGK | RSSSRNKTTT | 1020 |
| TYNTCTTCN | CCNMGNRWWG | SRAMNTGKTS | NSSGGGSGGC | | | 1060 |

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| AATTCGGCAC | GAGCTTCACC | AAAGAGCTGA | CATGCCGGGT | GATGCGACAT | CGCATCGAGG | 60 |
| GCAATACGGG | CATGGATGAN | CCGAANGGAN | TCTGGCGTTC | GCTCAACTGG | ATTACGGTTC | 120 |
| CCAAGGTGAA | ACGCTTTGCG | GCGAAAGATG | CGACGCTTAA | CTTGCGCTTC | CACCGTGCAA | 180 |
| TGTTNGTATG | GATGCTGGAA | CCGCGCTGAC | NGATAANGAA | TTCGCTGGTC | GCCGGGCACN | 240 |
| ATGGATGGTC | CKSTTTTCNC | TCCGCSGTTA | AATTGCSTGT | GCATCATCTG | GCAGGCTATG | 300 |
| TTCCCGCTAC | RCTGCAGCCC | ATCATGGATG | TGCGGCTAAC | GAANAAGTTA | TGACATGGCG | 360 |
| CAAGCGAMTC | GGGCATSCNC | GCGGCAMTTT | CGCAACCTGC | TGTGTNTGAA | GCGTMTCAAC | 420 |
| CGAATGCGGC | GCTYAAAAGC | NGGCTTGCGT | TGATTMMAAC | CNAACCCNTN | CNATYCTTTG | 480 |
| CCGNGNMNTG | CGTTCTCTCC | AACTCCGKKG | SYTGCCNCCG | TGAAACCCMA | CTNCCCCCCC | 540 |
| GTTGGACTTA | MRTNTTCAAA | AAMCGGMTNA | ACCSGAATNN | SAACCTNCCR | TCAAANTAMM | 600 |
| SAANTCGGGC | TTYGGGNRCC | CCCCNGAAYW | TTCKNCNGGG | GMNNTYCTCN | GGTTYNGGCG | 660 |
| SAAACNTTTG | CCRTNCYMN | TTTACAMGGC | NCMTNMTTGM | GGGSCSNNAS | GWCCCGGGKK | 720 |
| TNTTTNCAAW | TCNCNSKTTT | TTKGGGGGGG | GGCYGRTRMC | NCGGGCCCCC | GGCCCKKMAA | 780 |
| AAAAAMCMSA | RRCCNCYGGG | KKCCCCCCCM | NNATNGGGCG | YKCRAAACA | ACCCCAANRA | 840 |
| TNGNGMGGGC | SMACCSGNGN | GYNAAAKGGT | TSNSCTMANM | MKGMANNNCT | SGMSCCMNSN | 900 |
| NCTGMGGGKT | TTKGNNGARN | AANAMKMGGM | RCGNCGCENN | GAAAGGGSMS | GSCKSCNNGN | 960 |
| NGASNGWMGN | CRNNGANRCC | NCNGYGNMRN | NNGNNNGNNN | GGGRKNNACN | NMKMCAWSMC | 1020 |
| NSNMMGNNS | CGYMTNKCGB | | | | | 1040 |

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AATTCGGCAC | GAGACAANGG | CGTGAAATGG | GATCCGGCCG | AGCTGGGGCC | CGTCGTCAGC | 60 |
| GACCTGTTGG | CCAAGTCGCG | GCCGCCGGTT | CCGGTCTATG | GGGCCTAGTT | ATCTGCGCCG | 120 |
| AGCGTGAAC | TTCGGGCGAG | TTTTCGGCCG | TTTCTCGCCC | TGGCTTCACG | TTCGGCGAAG | 180 |
| TKGGGAACGG | TCAGGGTTTC | CAAACCACGA | TCGGGATCGT | GCGGTTCGGT | CAGGACTGGT | 240 |
| ANTCCTGATA | CTTKGGTACA | TCGTGACCAA | CTGTGGNCAA | TATTCGGCGC | GCTCCTCGTC | 300 |
| NGTCGCGTCC | CGCGCGGTAA | GGTCCANCAC | TTCTTTTTTC | TCGTGCCG | | 348 |

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

```

AATTCGGCAC GAGAGACCGG GTCGTTGACC AACGGACGCT TGGGCGCGGG CCCCTTGCGT    60
GGCATCAGCC CTTCTCCTTC TTAGCGCCGT AACGGCTGCG TGCCTGTTTG CGGTTCTTGA    120
CACCTGCGT ATCCAGCGAA CCGCGGATGA TCTTGTAGCG CACACCAGGC AGGTCCTTCA    180
CCCGGCCGCC GCGCACCAGC ACCATCGAGT GTCCTGCGAG GTTGTGGCCC TCGCCGGGAA    240
TGTACGCCGT GACCTCGAAC TGA CTCTGTC CTTACGCGG GCAACCTTCC GAAGCGCCGA    300
GTTTCGGCTTC TTCGGAGTGG TGGCTCGTGC CG                                     332

```

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

```

AATTCGGCAC RAGTCGGTCT AGACGGATTC AATGCTCCCG CGAGCACCTC GCCACTGCAC    60
ACCGTGCAGC AAAATGTGCT CAATGTGGTG AACGAGCCCT TCCAGACGCT CACCGGCCGC    120
CCGCTGATCG GCAACGGCGC CAACGGGACT CCTGGAACCG GGGCTGACGC GGGGCCGGCG    180
GGTGGCTGTT CGGCAACGGC GGCAACGGCG GGTCCGGGGC GAACGGAACC AACGGCGGGG    240
ACGTGGGGAC GCGCCCGGCG GGATTTCTTC GCACCGSSGC ACCGGCGGGG CCGGCGGCGT    300
CGCACAAACG CACCGGCGGG GACGCNGCGC CCGTNGGGCG GCTTCTKGAT GGGCTCCGGC    360
GGTNACGCGG CACGGCGGCG CCCGGCTCAC CGCCNGTTGG GACGCGGGGA CGCGTNACCC    420
CGATCTTCTT CCGCNCCCCG GAAACCGCGG GGCCGGCCCC ACATTAKACC CGGCGGNACC    480
GCGGMCCCGG CGGAACGGNG GGYNTTTTCC AACGGCGGGG CCGCGGAACC GNMGGSTGTT    540
CCTTNGGSGA AGGNCCAAKT CCCGKCTANC YYAATCCCCG ANGGKTGAMC CTSATGSNCA    600
MYTTMAGGAA CYTNCCANT KTTSGRACW CRCCNGGAAA ASRAWNKNGT KGGCAAACNA    660
NNTNICYTTKN NATTKGGNNA AAAANCCCTY CCWCSGRAC T NCCCCCNM GRGMCNNTNN    720
NTTTYGNCNN CCCGGSNAAM RNTTKATTTC NGGGGGNTCN GGGTKMNNNA AACCCCAAAM    780
MNRNNKCSCA ANGGGKSNGC NKNNMMNSGT TTTYCKNMRA MRNWTYKNKN NTCNGARSRN    840
NAAMCNSNK NGKKKNKAA ARNNTTWKTN KNSCNNNCN GRRNGVRGGC CKMKGSNMNG    900
MCWHNAWRNG NNGSNCNCKC NNMNAAAAA AASGGVNCKS NSMKNKKKKG NRGGGGGGGG    960
GG                                     962

```

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AATTCGGCAC | RAGAAGACGC | CCGAANGTTT | GCGCTGGCTC | TACAACTTCA | TCAARGCGCA | 60 |
| GGGGGAACGC | AACTTCGGCA | AGATCTACGT | TCGCTTCCCC | GAAGCGGTCT | CGATGCGCCA | 120 |
| GTACCTCGGC | GCACCGCACG | GCGAGCTGAC | CCAGGATCCG | GCCGCGAAAC | GGCTTGCGTT | 180 |
| GCAGAAGATG | TCGTTTCGAG | TGGCCTGGAG | GATTTTGCAN | GCGACGCCNG | TGACCGCGAC | 240 |
| GGGTTTGTG | TCCGCACTGC | TGCTCACCAC | CCGCGGCACC | GCGTTGACCT | CGACCAGCTG | 300 |
| CACCACTCGT | GCCGCTCGTG | CCG | | | | 323 |

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

| | | | | | | |
|-------------|-------------|------------|-------------|-------------|-------------|------|
| AATTCGCAGT | GTGTGTGGCG | GCGTCCAGAA | GAAGATGATC | GCGAACATCG | CCAGCGCCGG | 60 |
| CCAGGCTATG | GTGCCGGTGA | TGGCCGACCA | GCCGATCATC | ACCGGCATAC | AGCCGGCCGC | 120 |
| CCCACCCAC | ACCACGTTCT | GTGACGTGCG | TCGCTTGAGC | CAAAGCGTGT | AGACRAACAC | 180 |
| ATAAAACGCG | ACGGTGACCA | GGGCCAGCAC | CCCCGCCAGC | AGGTTTCGTGG | CGCACCATAG | 240 |
| CCAGAAGAAC | GAGATCACCG | TCNACGTCAC | CCGAGTGCCA | ACGCGTTTCG | GGTCGGCACC | 300 |
| GCTTCCC CGC | CCAAGGGCCG | GCGCGCGGTT | CGCTTCATCA | CCTTGTCGAT | ATCGGCGTCG | 360 |
| GCNACCAGTT | GAGCGTGTTG | GCGCCGGCGG | CSGCCATCAT | CCCGCCGACN | ANC GTGTTGA | 420 |
| GCATGAN CAG | CGGATGAATG | GCGCCGCGGC | TCGTGCCGCT | CGTGCCGAAT | TCAACTCCGT | 480 |
| CNACAACTTG | CGGNCGCACT | CGAACCCGGG | TGAATGAWTG | AATTTAAACC | GSTSAACANT | 540 |
| AACTACATAA | CCCTTGGGGG | CTCTTAACCG | GTYYTGAANG | GGTTTTTTGC | TTAAAGGAAG | 600 |
| AACYATTTCC | GGATANCTGG | CSTTNWTARC | GAAAAGGCCC | CRCCCATNGC | CCTCCACAGT | 660 |
| TTSCCCCTGA | ATGSSAATGG | MNCNCCYKNR | CNGGGNCTTT | AACRCSGGCG | GGNTTTTGKT | 720 |
| MCCCNCTKA | CNTTMMMTGC | ARNNCNGGCC | SKCCCTTCCCK | TNTYCCCTCC | NTCCCCCNST | 780 |
| TNCNGKTCCC | CNNAMNYTNW | ACGGGGGGCC | YTNGGGKCRM | TWTKKTTTGG | GCCCCMCCCC | 840 |
| MAAANASAA | NGGGKRN GTY | CSTTTGGCNC | CCCAMAARGG | NYCCCCCAM | YTNRRKMCSY | 900 |
| CNNTNKGGNN | CTGTNCKNCG | GAARAMAMCC | KCCCCGNSTS | STNGTYWAG | GNRWKGN SRG | 960 |
| CCSCCCCGGY | MNNNAAYAWN | WMNATNCNNS | STNANMAKKN | NNNNNNNSCN | WNGNGNNTCN | 1020 |
| SCNSNGGKBC | CSCC | | | | | 1034 |

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AATTCGGCAC | GAGCCACAT | CCGGGGCCGC | TCGTTGCATG | ACTCGTTCGT | CATCGTCGAC | 60 |
| RAGGCACAGT | CGCTGGAGCG | CAATGTGTTG | CTGACCGTGC | TGTCCCGGTT | GGGGACCGGT | 120 |
| TCCCGGGTGG | TGTTGACCCA | CGACATCGCC | CAGCGCGACA | ACCTGCGGGT | CGGCCGCCAC | 180 |
| GACGGGTCGC | CGCGGTGATC | GAGAAGCTCA | AAGGTCATCC | GTTGTTGCGC | CACATCACCT | 240 |
| TGCTGCGCAG | TGAGCGCTCG | CCGATCGCCG | CGCTGGTCAC | GAGATGCTCG | ANGAGATCAC | 300 |
| CGGGCCGCGC | TGAGTGCGCC | TCCGCGGAGC | A | | | 331 |

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|------|
| AATTCGGCAC | GAGATCGTCA | CCCTGGCGAC | CAGTGCACCC | AGGCCACGCC | ACCA GTTACG | 60 |
| GCTGATGGGC | CAGAAGATGG | ACCAGGTGCT | GGCCATCCCG | CCCACCGCAC | TGCAGCTGAG | 120 |
| CACCGGGATC | GCGGTCCTCA | GCTACGGCGA | TRAGCTGGTG | TTCGGCATCA | CCGCTGACTA | 180 |
| TGACGCCGCG | TCCGAAATGC | AGCAGCTGGT | CAACGGTATC | GAACTGGGTG | TGGCGCGTCT | 240 |
| GGTGGCGCTC | ANCGACAATT | CCGTGCTGCT | GTTTACAAGG | ATCGGCSTAA | GCGTTCATCC | 300 |
| CGCGCACTCC | CCANCGCCGC | GCGGCSGGGG | CGGCCCTCTG | TGCCGACCGC | CCGAGCGCGT | 360 |
| CACTGACGCC | ATCTCCGTCG | GCGTTAACCC | CGTGAGAAGG | TGGGTCGTGC | GCAAGTTGGG | 420 |
| CCCGGTCACC | ATCNATCCGC | GCCGCCATGA | CGCNGTGCTG | TTCCACACCA | CNTSNGACNC | 480 |
| CCCCCAGGAA | CTGGTCCGGC | AMTNCAGGAA | NTYCGTGTGG | GCACCNGCTT | CTTCCGKTRT | 540 |
| GGCYTAAACT | TCCNATSTTN | CSGCSGGCCT | CTGGCGTTNC | GNCCGGGCCG | NTCTTNCCAA | 600 |
| ATCGGSMMAA | ATCCCCANMC | AAACCCCCCG | GGTCTTGSGG | GCSGGGNGGC | GGCCNAWNCC | 660 |
| AAACCCCCCC | NTTAAANTCT | TTGKTNCCNN | CNCSGGCNCC | NCNAANSCAN | CCCTTTKGGC | 720 |
| NCTTCCCCCC | CCCAWTTTAA | CCGAKCGSCN | AAAYCCCAAGY | TMMGKCCYCY | KNAAAAAAAAA | 780 |
| AATTTGSCSG | CCCCAANTAA | ATTCCCNNGC | CCYTTGGGGG | CGRANCNYNT | TTTMCCSNSS | 840 |
| TKGNNAAMC | NGGANCCSGG | KAAYTMMTKG | NAAYCGCCSN | AAMBNTTTTC | TAANNCCCCN | 900 |
| YNCCCSGAAA | ATTNNAMAAM | CMNNKTGSNG | GGGKTTSTNC | SGKKGRAGGM | AAAAAANRSN | 960 |
| SKTTNMCNNN | SANMNCNSNN | SGGNSNNNNN | NNNCNCGYKC | CSNAANMCCC | CGCGGGGGGG | 1020 |
| CCMMCC | | | | | | 1026 |

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AATTCGGCAC | GAGAAGACGC | CCGARNGTST | GCGCTGGCTC | TACAACTTCA | TCAARGCGCA | 60 |
| NGGGGAACGC | AACTTCGGCA | AGATCTACGT | TCGCTTCCCC | GAAGCGGTCT | CGATGCGCCA | 120 |
| GTACCTCGGC | GCACCGCACG | GCGAGCTGAC | CCAGGATCCG | GCCGCGAAAC | GGCTTGCGTT | 180 |
| GCAGAAGATG | TCGTTGAGG | TGGCCTGGAN | GATTTTGCAN | GCGACGCCNG | TNACCGCGAC | 240 |
| GGGTTTKGTG | TCCGCACTGC | TGCTCACCAC | CCGCSGCACC | GCGTTGACGC | TCGACCAGCT | 300 |

GCACCACTCG TGCCGCTCGT GCCG

324

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|------|
| AATTCGGCAC | GANGCGTGCC | GCTNAACACC | AGCCCGCGGC | TGCCAGATAT | CCCGGACTCG | 60 |
| GTAGTGCCGC | CGGTGGCGTC | GTTGCTCTCC | TGACGGGGCG | CGGCGACCAT | AAGGTCGCTM | 120 |
| ATGCCCAGGT | AGCGGCCAG | GTGCATGGAG | TCGATGATGA | TGCGACTCTC | CAGCTCGCCG | 180 |
| ACCGGGAGCT | TGGCATCGGG | CCTGATCAGC | CAGGACGCGT | AGGACAAGTC | GATCGAATGC | 240 |
| ATAGTGGCCT | CCAGAGTGCC | CGTGCAATTC | CNGCGTGCTC | CACGGCAAAT | GCCTTGATTT | 300 |
| CTACTCCGCG | TANTGTTCCC | GCATCGCCTG | CGGGATGAAT | GGGAACCGCA | SGATGGCGAC | 360 |
| GAACGGGTCT | GANCTCAGGT | TTGCCGCTTT | GCGCACAGTG | GTCNACANCC | GGTACTCGGC | 420 |
| ATANATCTGG | CCCNAATCG | GCGCCGACGG | CGCCACNAT | AANAACGGGC | ACNACAATCG | 480 |
| CCGCCCCGGT | CACCCNAACA | ACANCTTGSC | ATCGGATTTT | GTCCCCANCG | CTCAANCCGT | 540 |
| CCCGAACGCC | TCNTCCGGCG | NACTTTTCTT | NNAWTAAC TG | CCGCTTCCGK | CCCTGGNGCA | 600 |
| WTAAATGGGA | AACCCTTNCC | CCACCTTGAA | GGGGTTGTTG | NATTTTTACT | GSTAACCCCG | 660 |
| AATTNTTCCG | GANTCGGTCN | KCCGGGSTTT | YSTNTTCCCC | ACCTTNGNAN | GGGCCGGCCA | 720 |
| AGSTTTTCTT | SYTGAAGGGG | GAAACCCAAC | TTTNTYTYYN | AACCSCMNAA | MYMTTTYCSG | 780 |
| MNAASCCNKT | CCCCTTTAAC | CAMGSGGTN | AACCGKTMNG | NGGKTAAGAA | GGGSKNNKTG | 840 |
| NCCCCYMANG | GGGGGRAAAA | TSTKTCNNCG | GGGCCKAAAW | ACMMMMYGN | GTGKKKNKSS | 900 |
| GCSAAATTTT | NMMRAACTKN | GGGGCCSSGA | NNTTTNAAAG | MSCCCCCSNN | GSTGKCCCN | 960 |
| NTTTCNNAA | WMKKGKNWNM | SNMNSCSNGG | GKYNSSGSNN | NNAAGMGGGG | | 1010 |

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| AATTCGGCAC | GANGCGTGCC | GCTNAACACC | AGCCCGCGGC | TGCCAGATAT | CCCGGACTCG | 60 |
| GTAGTGCCGC | CGGTGGCGTC | GTTGCTCTCC | TGACGGGGCG | CGGCGACCAT | AAGGTCGCTM | 120 |
| ATGCCCAGGT | AGCGGCCAG | GTGCATGGAG | TCGATGATGA | TGCGACTCTC | CAGCTCGCCG | 180 |
| ACCGGGAGCT | TGGCATCGGG | CCTGATCAGC | CAGGACGCGT | AGGACAAGTC | GATCGAATGC | 240 |
| ATAGTGGCCT | CCAGAGTGCC | CGTGCAATTC | CNGCGTGCTC | CACGGCAAAT | GCCTTGATTT | 300 |
| CTACTCCGCG | TANTGTTCCC | GCATCGCCTG | CGGGATGAAT | GGGAACCGCA | SGATGGCGAC | 360 |
| GAACGGGTCT | GANCTCAGGT | TTGCCGCTTT | GCGCACAGTG | GTCNACANCC | GGTACTCGGC | 420 |
| ATANATCTGG | CCCNAATCG | GCGCCGACGG | CGCCACNAT | AANAACGGGC | ACNACAATCG | 480 |
| CCGCCCCGGT | CACCCNAACA | ACANCTTGSC | ATCGGATTTT | GTCCCCANCG | CTCAANCCGT | 540 |
| CCCGAACGCC | TCNTCCGGCG | NACTTTTCTT | NNAWTAAC TG | CCGCTTCCGK | CCCTGGNGCA | 600 |
| WTAAATGGGA | AACCCTTNCC | CCACCTTGAA | GGGGTTGTTG | NATTTTTACT | GSTAACCCCG | 660 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| AATTNTTCCG | GANTCGGTCN | KCCGGGSTTT | YSTNTTCCCC | ACCTTNGNAN | GGGCCGGCCA | 720 |
| AGSTTTTCTT | SYTGAAGGGG | GAAACCCAAC | TTTNTYTYYN | AACCSCMNAA | MYMTTTYCSG | 780 |
| MNAASCCNKT | CCCCTTTAAC | CAMGGSGGTN | AACCGKTMNG | NGGKTAAAAA | GGGSKNNKTG | 840 |
| NCCCCYMANG | GGGGGAAAAA | TSTKTCNNCG | GGGCCKAAAW | ACMMMMYGN | GTGKKKNKSS | 900 |
| GCSAAATTTT | NMMRAACTKN | GGGGCCSSGA | NNTTTNAAAG | MSCCCCCSNN | GSTGKCCCN | 960 |
| NTTTCNNAA | WMKKGKNWNM | SNMNSCSNGG | GKYNSSGSNN | NNAAGMGGGG | | 1010 |

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| NGNGGGGWNS | NTCAYCAYCA | YCACSGGGYW | CWATTGCGGC | CGCAWCTTGT | MAASAGATCT | 60 |
| CGAAYTCGGC | AMGAGGGAMT | CKCTMGCNCC | GCTGTGCAAN | CCAATRAGGC | CTRATAATTY | 120 |
| CCACTCCACA | AAAAACCGTT | GTGTGTAYYT | SCCGRAAATR | AAGGCGCCGG | TNTCAACWYC | 180 |
| GCCGGTKTTY | CCRATYCCCG | TKTTGTAMCT | GCCKGGGTSR | AAAYCCCCGG | TGTTGGAYCC | 240 |
| CCGGATTGAA | ACTGCCGGKT | TGAAACTGCC | GKTTTSGCSA | TCCGGKWATT | GAMSTCRCGG | 300 |
| ATTAAAAAAC | CGGKKTGGN | GCTGSNCGTG | CCAAATNCGR | AYCCRATAYC | CCATGGCCTG | 360 |
| KYCTYCTCK | YCGGTACCCA | AAYCTGGGTA | TCCTATACTG | GYCCCTAAAK | GCAAWYCKGG | 420 |
| GCTGYCMMTK | TTGCKGGSgt | CCNAATTTAS | CACCASCgGT | TCCTTCCATA | CCNAAACNCG | 480 |
| CKTGGGCWCC | AGMCCGRAAA | AAAKAATAAT | RAKAAGGTG | CATNYCCAAA | ACCNCCGCCN | 540 |
| CCCNANTNCN | ATCCGNTNCC | MSCNCCCCCA | GCGGTNAAGK | TKSGGAAYTT | CTMMAACCCC | 600 |
| CAAANCCCCA | TAACNTNCGR | GAASAAACCC | CTYCNCGGGG | GYCNWNCAAA | ACASCNTTAT | 660 |
| TTGCTKSTTT | CGGGMWCCGT | GCCGCCNAAA | YCCCAAATA | CTTTYTGgGT | CCNAGAKAAA | 720 |
| ACCNCGGGCN | CCMCCCSNAA | NWTATYTCTT | KGGCAANCCC | CSAAACCTTR | TCMNACCNCk | 780 |
| ATRMTCCTT | CCCCVSCAAT | TGGYCGGRAT | NCGSNCCYTY | TCAAARKKSC | CAKWWNNNGN | 840 |
| GRRNACCMA | ACCCCAAGTY | CCMNAAAATN | GKCCCCGCTC | CNAACACGNK | TYYTCCSAAA | 900 |
| ASCCWCCCC | CCCCCCCRAA | AACCCCCCNA | RKANTNCCCA | AAAACNYNGK | GGCCCCCCCC | 960 |
| CAAAACMAAA | AMCCCCCSGM | RMACSGGGGN | NMCCCCGKKK | KKTTTTCTTT | TKCCMRSCCC | 1020 |
| AAMGCAMWSY | KSKTNMAAAA | GGAAGRANCN | TYCCSANANM | TCCCNWRSW | CCGSWGMGNA | 1080 |
| GAASMCCCC | CS | | | | | 1092 |

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| GGGGGGGNNN | NATACATCWT | CYGTGYACCG | GGGMTCTAKT | GGCGGGCCGC | AATCTNGTCA | 60 |
| ASAGATCTCT | NAMTTCGGGC | ACAAAAACTW | GACAAASYMT | CGNGCNMTCC | GTGTCCTNKA | 120 |
| TCGCAAAACG | NGTRACASAC | ASACACRTAT | GTGTGCCCCAC | CASCAAYTCK | TTGGGACCTC | 180 |
| GCTRACCGGY | TGCCCRNACG | CCACGYTGCS | CWTCTATCCC | RACGCCGGCC | ACGGGYGGGG | 240 |

| | | | | | | |
|------------|------------|-------------|-------------|-------------|------------|------|
| ATATTCCAGG | CACCACGCCC | AGTTTGGTGG | ACAATGCCCT | GGCAKTTTCC | TCRAANTTCG | 300 |
| TGAAACCGAA | TTCNSMTTGA | ACCNCCAARG | CCCCSNCCNR | AACARTTGGG | WTCCGCGGTT | 360 |
| CTCCCCACCG | KTTTCCGGGG | GTNTCGGCAN | AANCGCACCC | WTGGWTTCTM | TCNCCGCACC | 420 |
| GGGCGGACAA | NTCGGGTTGC | AATTTTGCRA | AYCGGGGCCG | GGATTCCSCA | AACGGGTGCC | 480 |
| GAAACTGTTY | YCRAAMACCG | GGAKCCGCAA | TTTCCGGGCR | ANAAATTCN | YCNCACCACT | 540 |
| GCTTRTACTT | CCCCGACCGT | AACMANTTTC | ATCGTCNTNN | CCTCTGCCT | TGGGGCAGGG | 600 |
| CKAAAYACCG | CMTTKGGTTT | CGCAACCTGC | GGCCCAANTC | CCNAMCCRCA | CTTTCNATTT | 660 |
| GGNTCGAATT | SCCCCCCGGT | RANAACCSCC | NTGGCCNNYT | CGGASSAAAA | NGGGCCCTNT | 720 |
| KGGCNSCCCC | AGTAANACCC | TACCNAYTS | CAWTC'TTTGC | CAAAS'TTKGG | ACGAANSKTG | 780 |
| GGNTTCCGGK | ATTTYTTTGS | GGNCNCCCTN | TATNGGSNTN | GGGCCCKCYN | NCSTKTGKCA | 840 |
| NASSKAYCCS | NGNKGGGGGT | ACCCCCCTMG | GGGGGTTTTT | NSSGCCCCC | AWAYGNKSTG | 900 |
| GCCCCNNGG | GGAAKAATWT | MWWTMCNSGG | GGGAAWTTTT | NTSTGGAMCS | SGGACYCCCR | 960 |
| GGGGGKTTTT | TCCCCCNCSA | NNAWANGGGG | GGGGGANAYT | NTGNSGNGGG | KWNTTTATTT | 1020 |
| YTYCYCCTM | TKACMSGGGG | GTTT'KKAKNG | GGGGGAGAAA | ANAAAAAAA | RAKGGYKNTT | 1080 |
| TSKNCACNCT | GKWNWNWANR | NAGAGKTCCT | CKCKCCNCSG | SN'TTCTTTT | MGNSGSYGGG | 1140 |
| GNNGNNNAAA | ACNKSRMMAC | KCSYTYCCCG | CGYCTCCTCC | NCNGGGGYGS | NGSCGNSTYN | 1200 |
| GNNKGRKWT | TNTMGNCGTN | SCCTCCNCCC | GCKNKNTGTC | TMTCNMYGSG | C | 1251 |

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

| | | | | | | |
|-------------|------------|------------|-------------|------------|-------------|------|
| AAATCGGCAC | MGAGTATCAC | CAAKCTGYGT | GGCCAGCAA | AGTGGAGCTA | TTACTACCTG | 60 |
| TATGTGATCC | TCRACATCTY | CTCCCGCTAC | KTGGTCGGGT | GGATGGTGGC | CTCGCKTGAK | 120 |
| TCRAAGGTCT | TGGCCRAACG | GCTGATCGCG | CAAACCC'TTG | CGCCCAGCAC | ATCAKCGCCG | 180 |
| AACAGCTGAC | CTGCMCGCCG | ACCGGGGGYC | GNCAATAACT | CCAAACCGGT | GGCMCTGCTG | 240 |
| CTGGCCNACY | CCGTGTCCCA | ANTCGAACTC | ASCCSGCNMA | CCAKMAACKA | NAACCGTTGT | 300 |
| CTGAAGCCCA | GTTCAAAAAC | CTCAAGTWCC | GGCCCRAC'TT | CCCGAAACGG | TNCGAGTCKA | 360 |
| TCSRAGGSGG | CCGGGTGCMC | TGCAACCGGT | TCTTCGGNTG | GTRCAMCCCN | AAAMCAAGCA | 420 |
| TTCCGGGMTC | CGMMTGCCCA | CGCCGCCAAS | TTTMCTACGG | GCSGSCCNAT | CAAATTCGCC | 480 |
| GGGAACSGSN | CCMCKTCNK | GGAMACGCCC | TWCCAAAACC | CYCGAACGGK | ATCCT'TCKGY | 540 |
| NAACNCCCGA | RCNCCCKSKT | TCCGGGCTTC | NMSGCGAATA | CCCKNSCMNT | CCGAATCCAA | 600 |
| TTCCCMKYGG | CTTTTYYYCC | CCCCGGCCCC | AAAYNGGGYC | CCTASSNMKC | KNCCAMNANT | 660 |
| CCNWATCTGG | NGGTCCCNAN | KYYGGCGTTC | NMAATSAMNA | NMNRGGGTYT | TSCYACMMN | 720 |
| AACCGKNNKG | KCCCCMKCTK | MANAAAKATT | RATCAMKWNG | GGNKCKCNCN | NAAMACCSCN | 780 |
| CNCYNCWYTC | TMYCSSKWGC | GCSMYNANCA | SNGGGGAGGW | GGSGRMKMCT | CTMTCTCNCT | 840 |
| MCGGCCKN'TN | TYCKSGAKAT | ACASMNKTCC | GCGCNGCGCN | MAAMANRAKA | CTAKCCGYGN | 900 |
| CCSNSTMTYN | CTSNNMKMNN | TCCWMWNATC | NTYYGKKCNN | KCTMKATNWC | CSCTSKCNCK | 960 |
| MRAMTCKTYG | SNMTCTTCCA | TCNCTCKKSC | SNMSKNTCKC | KSCNCCNCWN | CNKCNMKCWN | 1020 |
| GGNSTCRCCY | TCTMNNNTCS | AGCKCGSKNC | WACNCACACK | NGWCTYTTCC | WKNNMKCNKM | 1080 |
| TCKCKCACRG | MTMTCWCCS | | | | | 1099 |

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GNGNTATACA | TCWCTGTGYA | CCSAGGATCW | ANTGCGGCCG | MAAKCTWSTM | CASAGATCTC | 60 |
| AAAYTCTGCA | MGAGCGGCAC | AKAKYSTCGT | CCMRACCCGG | CAYACWCCWG | CNCGCCCCWT | 120 |
| CTTRGACCGG | GGCKATASMC | ACCGTTGGCC | CCGGCNCGCA | CCTACACCAC | CCACGCCGCC | 180 |
| AGCGCCCCCW | TRAMCAAACC | ACCCCGCKTT | TACCGCCCGC | GCCGCCGGGG | CCACCACCAG | 240 |
| CCCCACCGGC | ACCACCGGCG | CCGCCGTTGC | CAAAACAGGC | CCGCKTTTGC | CACCRA | 296 |

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1073 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|------|
| NGNGSGNKMY | ATCATCWTTT | TGCACCSNGG | MTCWATTGCG | GCCGCAATCT | TSTMNASAGA | 60 |
| TCTCGAAYTC | GGCAMPARCA | TCTGCGCGGN | GAATGTCCAA | AWGTCWKTA | CGGCMATCGG | 120 |
| TTTGCCGYCA | ACCACKCTRT | SCAKATGCGG | GCCAMWTYCA | AACCRATTAT | TTGGGYCGAG | 180 |
| AAAATTMCG | CKTGTRASCA | ACCTGCAGCG | GGTCAASCAA | CAGCCTCTRA | ACCGTAAATY | 240 |
| CKTAGGTNKT | YCCGGCAACA | ASCYCRATA | TSCGGCCCGC | AMCCACAAAA | CCTGANTNGT | 300 |
| TNTTCNCRAA | NCCGGTYCCC | GRAGGGGTS | ACTGCSGTAR | GCTTNTCWYC | NCCTTRACAT | 360 |
| TAAACCCCC | CGGNTCWTCG | CCGCGCCCAA | ATYCYTGCCC | WTKGCNACCA | YCCCANCTTG | 420 |
| CSGTATGGTS | RAANCASTSG | GCRAACGGTM | MCCSTACCKC | TGGCTGATYC | KTCGGNTCCS | 480 |
| SNAATTCGGG | GATTTACGGS | CAMGGTTAAY | CCAGGYCCCC | TNTGCTCKY | CNACAACCSG | 540 |
| ATCMWCNCCG | TACCTKTTAA | AATTCTTTGT | GGTGGAACCC | AWYCKAAAAA | NMTNTYCCCN | 600 |
| TCCAMGGGG | CYCGGAAKKT | CNACNTGGKT | NACCCCTNCC | YTTGAASTTT | TCYTGNCCTC | 660 |
| GGCCCKAAAS | ANACCSGAKC | CCCGGAAYCS | WTAGGCYTCN | TGCCCCSTTA | AATTKGNCYC | 720 |
| AATCCKCCAA | CGCTCCCCGG | GGTCSSCMT | TAAAMTTCCC | CCCKSCASNG | GAATYCYKSG | 780 |
| GCWGTMTATW | CCNCCCNNTT | CYYGKNAAAC | SCCCCCWKGN | GSCTYCCCN | SNTTSSGCCS | 840 |
| GGTTS GAMYC | AAAAWTNGGG | MMCNRAGNCG | SGNAMCCSCN | GKKGGGSATW | TKAAYCYGG | 900 |
| GGGGGTCNYC | CCCCRCSNAA | AAGYGTGKGC | KCCSSSCCYC | CCMARTTTYT | CNGGMRCMAM | 960 |
| ACCANGGGNG | CTCCCGTNCW | WGGCTCCCSN | SNSMAMAAAN | NKCKCKKGGG | CKGARRNMNA | 1020 |
| MCTCSNGNGG | WTCCCKNKTC | NSCNSGNCGS | YGGNSASWCC | YNYCNCCACA | ANC | 1073 |

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1166 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|------|
| CGCCCCGTTT | TTMMTTTCA | TCATTACCG | GGMTCTAGTG | CGGCCGCAAK | CTTGTCACAA | 60 |
| GATCTCGAAY | TCGGCAGAS | ACAATSTCGG | GTKGGGCAAT | GTCNGGTGGG | GCAACTTTGG | 120 |
| GCTCGGRAAT | YCGGGGTAA | CGCCGGGTCT | RATGGGTSTG | GGTAATATCG | GGTTTGGTAA | 180 |
| TGCCGGCAGC | TACAATTTCT | GTTTGGCAAA | ATATGGGTGT | GGGCAATATN | GGGTYCGCTA | 240 |
| ACACCGSCAS | TGGRAATTYC | GGTATTSSGT | NACCGGTRAY | AACTGACCG | GGTNCGGTGG | 300 |
| TTYCAATACC | GGTAACGGGA | ATGTSGGTTS | YYYACYCCGS | GSAACGGNWW | YTTNGKTCCT | 360 |
| TMMCNTSSM | CCKSAAMTSM | KMGSTSTYCT | MTYCNNGGAS | TAMTYNMCCC | CCGWAYCKSC | 420 |
| WAYCCCTCGT | CATYCCMCMC | SGSGYCCTCA | MNCCACCYTG | NGYYCCCTCC | MKMTCTCYAYT | 480 |
| CMNTCCGGTW | CCTNTMMNCC | CSCNCRYCTC | AMCNCTKSGK | CACCNATMYC | CSACKCHTCT | 540 |
| MCYMCSCAKN | MTCCCTCTCN | CCTYTNNCCA | MCMCSCCTCTM | TCMAACTCKC | CCGGYCKCNC | 600 |
| MYCTCTCKCC | AYNMAACCKK | TYCYWCNWC | YMYCKCKCAG | WYKNMCTCCW | ACTCTMYNTT | 660 |
| TCTCTCNKCC | CMKACCKNTT | CTCWCSCCCC | CCACAKAYMC | YAWCMTMTCC | MCTCKACSCC | 720 |
| CYYCNNYCCM | NMCWCMTCWC | TWNAKCANCN | TTCTTCTCTC | MMYMTMACKC | WCNNTCNCKK | 780 |
| SGACCTCTC | ACTKMKCKKM | TCTCCTTMCK | CCYMWCNCTC | MKYNCCCTCC | NMTCMTCKYT | 840 |
| CCTCNCNMRY | CYYAKCAKC | NMCTCCCCAN | KMCACTKCT | CCCCAKMKS | ACNCKCCCWC | 900 |
| CCTCCTATCC | WCTCTCWCTY | ATCTCKCTCW | CNYCMYKMC | ACNCKCYAYT | CNACTMNMWN | 960 |
| CCANCNTCT | CTNYCTCWCK | ACGTYCKCKK | CTMCKCNMYC | NRWCTYRCCT | CKKCCNCCRN | 1020 |
| CKNMCCKCTM | CTCTCCWMKM | TCCCWCCCAT | CTMMKSTCTC | WCNMTCCCT | CNKCCYNYNT | 1080 |
| KCYTYCCMYG | CTTCKNTCMT | MCCWCCYATC | TCTMKCCTCT | CWCACYMCAC | WMTTACWNCC | 1140 |
| ACTCTCTRCW | CKCKCMCCR | MTCTCB | | | | 1160 |

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|------|
| NGNGGNNNT | CWTACATCWN | TCTNCACCSG | NGMTCWATTG | CGCGCCGCAW | NCTTGTMNAS | 60 |
| AGAATCTCNN | AAYTCGGCAC | ANATGTCTTT | TSTMTAKTGT | GGCGGGGNGC | CACGCCKTAT | 120 |
| GTGYGCCTGG | GYTRACCCAA | CCCCGCGGCS | CGGGCCRACC | AGGCGGGGRA | TSCAGGCCGC | 180 |
| GGCGGCCGCG | GCGGYTATAT | RAAGCGCCGY | TTTCKTRATA | ACGGTSCCGC | CGCCGGGTRA | 240 |
| TTACGGGCAA | AAYCGGKKT | TTGGGTRTAT | AACGCTAATT | GCAACCAWTT | TTTYCGGGTC | 300 |
| AAAAACYCGG | CGWGCANATC | NCGGGYCNCT | RAGGCGCATT | YMCGCCAAAA | WTNTGGGCGC | 360 |
| AAAACCCCKT | TSYTATTTTN | TGGGCTATSC | GGYTGCTTCG | GCAAACGCTY | CCCGGGTTAA | 420 |
| TCCCKTCCGC | GGCGCCGCCN | AAAAACCACC | AATYCCGYTG | GGGGTGKYCC | CMCAGGCSGT | 480 |
| TGCTYCGNGY | CACCTGGCCA | AAAYCCCAWT | AKATTGGGTG | SCYCKTSCGG | TTSYTGGGCY | 540 |
| CAATTACCCC | CNCGGGNAAA | GRRAAANAA | ATCNTCCNTT | TGCTCGGYCA | YCTTTMTTGG | 600 |
| SAAAAGGGGC | ATGGCSCGGT | TYTTTACCT | CAAYCCCNNA | NCANTWACCT | YTCCSCCCGG | 660 |
| GGGGNCANAA | CGSTTNGCTC | CGSGGNAKCC | TKGTMCCCGN | ATCNAAAGGC | CNGAATTTGG | 720 |
| TYYSSTYCN | ATTWTWKKKY | CCCCWCNTTG | YAAAAAKCCA | AAASAKCCCK | YCNAMMYKT | 780 |
| NGGGGTYS | GCKNYCTTK | SNMTTAAACC | CYCCCCAAAA | YNSGGGKKT | TCCGCYNSAT | 840 |
| KCCACCNCCK | GNCGGGGNA | SAAAAAAAY | TTTTYCCSAAA | ATCCCACCYY | TCYKTKSTRY | 900 |
| AMACCCCTT | TYYMKKAYTC | CKYSCNATTC | SGMTTCWAAA | TYCCGYGGCT | TNTTCCCCCK | 960 |
| CSGGNGCCCC | AAWTTTGKTT | YNCNANTTYC | CCCNAAAMNCM | AWTMGGGGKS | KCCATTCTGG | 1020 |
| SCYTMAANTA | AAANAANGGG | NKTTTTYCTY | MANAAACACN | GTGKCNCCN | CNAAMAAASN | 1080 |
| AKMAAAKAGN | KKKMTKNNSA | AANCCNCCCC | CTSTYNTYTT | NKTNMCKCC | CYGGKKKNKGM | 1140 |
| SWSWYNTTCT | NCCCRCCCCC | YNYNKTGANA | AAMNCCYCCS | GGSTMCRNAN | ASNMTTTTCK | 1200 |
| STSTNGMGCC | KMBASNANAN | MCAMWKWYCC | | | | 1230 |

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

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NGNGGGKNNNA TMAYCWTCTC ACSSGGTCTA TCGGGCGCAW CTMGTMMAASA GATCTCNAAY      60
TCGGCAMPNAN GCATMTCMMC CATATATAAC CATTGCGTCS GYWTGCAWCT CRAAWCTGTC      120
CTTCSKGCCG TTKTACRAAG GTGGMWTGYT CWTYCCTRAA SCCCTCRATC TCKTKTATYC      180
CTKGGGCTYC ACTTTAACSG RATKSCTGCC TTKTAYCATT RATGCAAWTA WTGGYCRAWT      240
KTTGCAGGCC RACGGCWYCT TTTYCCGCRA GRACAATNGA TTGGAWYCGC TYCGCRAGGC      300
CCGGCACCAR ACCGGGCNCC AAAGGYCCGC GCAAWTSCCT GGKTCAAAAA TGGTGCAAAC      360
AAAMCNATCC CCGGYTTRAC CGCAGYTAMC ACAAKAAAAA TCCCWTTGGCC GCACCAWNNT      420
TTYCRATCWY CWYCCCCACC TTRAACCTGK YTGCSGTATT GCCTKCCTGC CTCRACAGCM      480
YCNCCKTCA AACCTGCGGT GACTCCAAC TGGTCTGGYCG AASGGGGGYT CAMCGGACAA      540
AACCCCRANN TCGCCAAATT TTCNCCCCC CYCGGGAAAN GKTGATMTTC TCSNAACCSA      600
CMGGGNNTW NAACCTGAA CSSSGSNKGA MYNSCCSGGA ANTTTTCCCT TYNGGGCGRN      660
AAANCCTTTT AAGGTACCCC KGGNGGGGKG CCCYTTTGGG AAAACAACCC CKATTGGKTT      720
TGGAAATNTT TKCNCCCCCA TTCNSGGGGG GGGCCCCAMC CMMCTTTTN TCMSCNMTYY      780
YCYGGGAAT TNYTCGCCSG GAAYYCGGSM CCKGYCCTAA NCCCCMNWGG GKYSTGSNAR      840
GGRATMAWWT TYSTTTYMC CCGGCNNCCC CCKAKMCNT KGNTGAACMA AAKCSGGGG      900
GSCNMYMWYY YCNNGNRTT TNRGSSNMT TYMAAMMAN GGGGKYWTYY CKCCNGSCNN      960
GKTYSGGGST TTTCNTTTS GGGSSATYKG MACCCCKTMT AYCCGGGGGT NTKTKYCCCC     1020
SC                                                                    1022

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(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

```

NNCGNNKNTA TAMAYCWYCT NCACCSGGGA TCWATTGCGG CCGCAATCTT STMAASAGAT      60
CTCKAAYTCG GCAMGANCCG CAWCTATTTG KGTGRASCGC ACCAGCGRGA CCTCGCSGKT      120
CKTTYCTTGC AGRGAGGCCCK TGGGTGGCRC CGGTGGCAAT GCCAACCGCC CCCCCAACN      180
CCGCAAATMY CRAAAAACAA CCCSGGGGTA GKTCCSGGCC GCCAAATMAA TAACCGTKTT      240
AACKCAGGCN ACGGCCAACC GGYCCCGCCC AACCAAGCNA CCTCCCCSCC NATAGGYCCG      300
GTGGGGGCTC CCKTATYKCC AASTCGTCAY CTCNACGGGM CGGYCCMCWT TCCGCCTCAT      360
CCGTCTCTCC TTMMATTTTC CRTCCACYKG GCGGGGAACY TTTTNYCNC CCTTGSCMAN      420
CACCNAAAGGY CNAAAATTNC CCMTGCCKYG SNNCAAAYGR GATTGGGGTY CGKKTNTNT      480
TCNMCCMAAC CCCCNTTTNA CGCCCCMATC CCYTWATACC CCCWWMCMNS ANGKTTGNSA      540
AAKTNNCCCC AAATRCCAA MTTCTTCGCC NTTMTFWMCY YYCCTTTCCC CMCCWNAAA      600
GGSCCRCCYY TCGGGAANTY TCCCNCAAA AWTCAMWCCM TTTCCNCCA AGAAWTTCSG      660

```

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|------|
| SACTCCTTTN | TTCNNGGNAM | ATANATYYTT | YCKTNGGGSK | TTCCGMTNCN | AMMAATNTCC | 720 |
| RGGGKAAMCC | AGKNTNNTCC | YYYYCCCCAA | NNTYCCYKGG | RM CYNNYYCY | TTAAANRASR | 780 |
| SAACCKSGG | GKCYNCNCSS | TARCCCCCAM | KAAAATTTCC | CCSSKTTTC | TYYNKKMRW | 840 |
| CCCCCSAAM | ACTMTWAYTT | TCCCKCGNNN | TTTSYCKCS | KCAMWMMTG | KKNCTTTTTT | 900 |
| YCSMATAMA | CTTNGGKCCT | NTCNYGSGCG | CMAAANAAGG | CGCGSTTCTN | TTWMMAMACA | 960 |
| YNTSGNMMA | SAAKAKWATA | AWNNTKKYK | TKNNCCCNCC | CKCKCTTSNN | TNKKCMCSKS | 1020 |
| GGGKNWNKKR | GWCTCCWCNC | CKCCNCKNK | CKKWATMCCC | CCCCSKCCGM | NCMNNTTTKT | 1080 |
| CCC | | | | | | 1083 |

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1069 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|------|
| GGGNNKYAT | MCAYCWTCTS | YACSGGMNC | TATTGCGGCC | GCAWYTNMTM | GASAGATCTC | 60 |
| GAAYTCGGCA | MGAAAAAGW | GATGTGCTGG | ACCTTMCCGC | GCGGGACGCR | ACCRACAAAG | 120 |
| RAASCGCGCC | ANAATATTGG | CCACAKTTGG | TCACATATTT | ACCCAATTMT | AYCAGGGAYT | 180 |
| MCCATTCKKG | GGACCRACCG | CACAATCCCR | ATSKTGGTTT | GCRAACCCTR | ACCGTCCCCA | 240 |
| MYTYCGCCRA | STTGAACCAG | GGCRAAAAA | CGGCCRAAWY | CTCGCCCTGA | NTCCCGCTCS | 300 |
| GCGCNAATAA | CTAGGCCCAT | TKAACGGAAC | CGGNGGCCSC | NANTTGGCCA | ACAGGTCCTR | 360 |
| ACAAAGGGGC | CCCASYCGG | CCGGWTCCCW | TTYCACNCCC | TNKTCTCKTG | CCGAATYCGG | 420 |
| WTCCRATNYC | CCWTGGGCCT | TKTCKYCKYC | KYCGGTNCCA | AWTCTNGGTA | TNCTATRGKG | 480 |
| TCCCTAAAT | SCANATCTGG | GCKYCCATTT | NCTGGSNTTC | NATTTAMMAN | SRRCGGTTCT | 540 |
| TTCWTTCCRA | AACCGSNTGG | GGCCNMCCA | AAAAATGATN | ATAATAATGK | YGSCTTTCAA | 600 |
| ACCCGCCCCC | CCCATTCTRW | CSGTTCCANC | CCCCNGNGGT | TAAGKTGGGA | ATTTYTNAMC | 660 |
| YCNARGCCCT | NATTTSGGNA | AAAACCYCIC | GGGYCTCAAA | CMNYTTTTTT | GSKSSNTCGG | 720 |
| GCTCRTTCSC | CAAAACCCAA | ATTNTYNYGG | GGYCKTNAA | ACMCGGYCRC | RCCGGAATTT | 780 |
| TTTTYTGGTTC | AACCCCAACC | TTTTCAASCC | NTTTTYTYTT | TRCCSSCSMN | TNGSSGGGNT | 840 |
| KSSCNTTTCY | RARKCCNMN | GGGGGWYCYN | CCCCRMNTTT | CTTTTTTTTT | CCGTNNMAAM | 900 |
| NGKTTCTTCA | AASMCCCCC | SCCCCCNSAA | CCCCCTNAR | GTTTTYCMMA | AANNWYMNNG | 960 |
| KNCCCCCCCC | MMNAAAAAY | YSCCCGNRN | ACSMNNGGGA | MCCCCCGGSN | NTTRKTTTTT | 1020 |
| TNCMSGYCCC | CSRMASYTTT | TKAMAMANRR | GAMNSMTTTY | TNNRGNWNK | | 1069 |

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| NGNGGGGKWK | MATACATCWT | TCTTCACGSG | GGATCWATTG | CGGGCCGCAW | TCTNGTMCAA | 60 |
| SAGATCTCGA | TYTCGGGCAM | NACCCACCWC | TCCRAAAAAA | ACCRAAWCT | CGGGSKCTYC | 120 |
| GARAAGTGTT | GCCCGCKTTR | AATTTAACAA | ATTCACTGTC | ANAGTGTCAC | GGCKTTACWT | 180 |

| | | | | | | |
|------------|-------------|------------|------------|-------------|-------------|------|
| YCCCGGCAAA | GGGGCCACAA | CCTGCAGRGA | SCACYCRATG | GKTGYTGKTS | CNCGGGCGGG | 240 |
| CCGGKTNAAG | GGACCTGCCT | GGGTKTGCSC | TMCAAANATC | WYCCGCGGGT | YCGCTGGRAT | 300 |
| MCNCAGGGGT | GTCAAAAAAC | CGCAAACAGG | CACSCCANCC | NTTTACGGGS | CTTAAAANGA | 360 |
| AAAAGGGCTG | ATGCCCCCAA | GGGGGCCCGC | NCCCAACCTT | CCGTTGGTCA | ACAACCCGGT | 420 |
| CTCTCKTGCC | RAATCCGRWT | CCRATNYCNC | CWTGGCCTTK | TCKYCTYCTY | CGGTACCCAA | 480 |
| ATCTGGGTAT | CCTATASTGT | CCCCTAAWTT | CCAAATCTGG | GCTGTCCAAT | TSCTTGGCNT | 540 |
| TCCAAATTTA | CCANCAACGG | TTTCTTNCAT | NCCAAAAACC | GNTKGGCKCC | NRACCCRAAA | 600 |
| AAATGAATAA | TAATAANNGG | KCNNTTYCNA | ACCNCCCCC | CCCNATTCCA | TYSNGTTCCA | 660 |
| NMNCCCCCAG | NGGKTAGGTK | GGGAAANYYC | TCMACCYCA | ANCCCTWARS | TTTTNGRAAT | 720 |
| KAAACCCTYC | YCNGGGTCWW | TYMAAAAAMA | NTTATTTGGN | NGNTTTCGGG | MWNCKRKNST | 780 |
| SCCAAATCC | MAAATANTTT | YYTGGTYCNA | TWAAAAAMCG | YGNCMNCCC | GGAAAAWTTT | 840 |
| TTNTGKTTSA | ACCCCAAAAC | YTTTTCMNAA | NCSSKTTTTY | CYTTCCCCC | AMNWTGGGYS | 900 |
| GGGNATKGYG | SCYTNTCTTA | TKTKYTYMTW | CMGGGGGGNN | MKMTCCMMCCC | CCMTTTYCY | 960 |
| NYWRTTTTTN | KCCCCCKTNMR | NNRAANNGGN | YTCSYNANAA | AAGCNCCCC | SCCKNCCCNA | 1020 |
| AAAAWCCCCN | NMNARAKTNT | TTMKANNRMN | SCKCNKNGKY | YCCCCCCCWC | YNMNNAAAAA | 1080 |
| AATMYCCNCC | RASANMCASM | NMGGRGNRSC | CCCCCCCSTT | NNNNTMTTNT | TTTTTTCSTRA | 1140 |
| GAGCKCCSCG | MNNANMKNCK | CTTTTTKCN | NNGNNGNGNN | GGNGMNCKCC | CCNAGAAAMWK | 1200 |
| CTKSTCCCKS | | | | | | 1210 |

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

| | | | | | | |
|------------|------------|-------------|------------|------------|-------------|------|
| NGSSSNGNNA | TMCATCWYCT | GYACSGGGMT | CWATTGCGGC | CGCAACTNGT | MAASAGATCT | 60 |
| CGAAYTCGGC | AAKANACACC | ACCGCCGTGT | MTATACACCG | CAAATGTTCT | GKKTGCCAAA | 120 |
| ACCGAGACGC | GCCGGCCGCG | GGGYTCCAAC | GCKTTACYTR | ACCCGCCAGY | TCAGTGTTTRA | 180 |
| AACCGGTGYT | RAGGGCCGCA | CCCAACWTAA | ACGCTTTAKC | CAAGRAWYTG | GKTGGCCCGC | 240 |
| AGCCACCTGY | TGTGGYTGCC | CTCWYCGGTG | GTAGCGCCGG | TTANCGCCGG | TTGCGCGYTC | 300 |
| AMCASCSCGC | CGGTRATCCC | AKCNWTCCCC | CGGCCMRACC | CACCGGGCAC | TTTGRACGGT | 360 |
| GCCGCCAATT | CAAAYCKYCT | GRWTCCTTCM | AAACACCACR | AAGGCCACCM | CCMSCACCNA | 420 |
| ATMGGGRACT | TTAAGGCCCA | GGCAAAACCT | NTRAKNCCT | CCCGGGCRAA | GGTCCSGCAA | 480 |
| SCRATCCMAA | AAAAKCKNAT | TTCCCCCAGC | AKCAACCCAA | MMCGSTTTGC | TGCTTCCGGA | 540 |
| TTCGAAMCCA | ATTMCWGGKT | NCNWGGGAAA | AACASCNNCC | NWTAKCCMGG | CCCMCGGGCA | 600 |
| ATTTCSGRAA | SAACCCCTNY | CCCGGGTTTT | YCCTGCTCMG | GCCCAANACC | CCCGGGAATC | 660 |
| AAAAASGGTC | GGNCAAANGG | GCMAAACCSC | SACCCMACTT | WTTCCRCTTN | GGGGGGSCWN | 720 |
| CKKNGTTTAA | AWKSCCTCY | CTSCCCAAAY | TCGGKCMAAA | NNGRKTTGK | TTNGGCNACC | 780 |
| NTTTCGGK | CCGGGKGK | WGKYCTMNMA | CSTTTNTTTT | SCCCCYKAAA | NYSCCCCCC | 840 |
| CGGSSCCCCG | CCCGGGGGGA | NNTTTTTTAMA | GKKTYYCCCT | CCCCAMAAAA | ANACCCCN | 900 |
| CCSGGSCCCT | TTKRWAAAMN | KCTSCCCNG | GNNGGGGKCM | GGKTTATTMT | NNNCCSCC | 960 |
| TCCGCGSAAA | AAATAKMTT | SYCCCCCNC | CTCKKNCKNR | GKAMSMSCGC | TCCCYCTCNC | 1020 |
| GCNKNTWAAN | ARSNCCKKNN | CCNCKKCCGS | NSNGKCNWCD | NCCSTSSNCT | NKGCNCKNCN | 1080 |
| KAAANAAYNC | NGSMSTSSMN | CNKCC | | | | 1105 |

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| NGSNSNKNNN | TAMAYCWYYC | TSCACSNNGA | ACWANTGCGG | CCRMWCTNS | TMKASAGATC | 60 |
| TMGAAYTCGG | CAAGAGCGGC | AAGAGTGTGT | GCATCTGGTC | ANAGTSTMMA | CRCGGTGCCG | 120 |
| CSGGTGKGR | GASCACMCAT | NTGCGRACAC | CAAACCKTC | GCGGGYCACC | GGCKTCGCC | 180 |
| GCAAAYCCT | CCAGGCCACC | TCRAACAAW | YCTYCTGCAA | CGCARGCCGT | TYCGCGGCCG | 240 |
| RATCCTGGKT | CASYYCGCK | TGCGGTGCCC | AAGKTACTGG | CSCAYCAAAA | CCGCTCCGGG | 300 |
| RAACRAACKT | AAWYTGCCG | AATTTCNTTC | CCCTGCGCCT | TGATAAATTT | NTNAAGCCAC | 360 |
| CGCAAMCCTY | CGGGCKTCTC | CTCKTGCCRA | ATYCGRWTCC | RATAYCGCCA | TGGCCTNKTC | 420 |
| KYCTYCKYCS | GTACCCAAAT | CTTGGGTATC | CTATANTKYC | CCWAAANRCA | AWTCTGGGCK | 480 |
| KTCCATKTSC | TGGSKTCCRA | ATTTAMMACA | NCGGTTTCTT | TCWTACCAAA | AACCSNTGGG | 540 |
| CCCCRACCRA | AAAAGGATAA | TAATAAKGTG | CWWWCAAAAC | CCCCCCCCCC | RRTTCAAYCG | 600 |
| GTCCARCACC | CCANGNGGTN | AGGTNGGAAT | TYTMAACCCC | CAGCCCATAA | SNTTNSGNAA | 660 |
| AAACCCCCCN | GGGYMYCAAA | AMMCTTTTTG | GGGMTTCSGS | CCATKGYKCC | AAAACCAAAA | 720 |
| TMTTTCYGGT | CRWAAAAACC | GGCCNCNCCG | NAAATTTTTT | GKCAACCCCA | AACCTTTMAM | 780 |
| CCNNNTTCYY | YCCCNACAA | TNGSGGNKN | NGSSCNTTYT | TWTTTYYNNA | GGGGGRRWC | 840 |
| SNCCCCNAAN | YYCCNAANKG | NKCCCGSNMA | AAAGAGANTT | YCMKAAAAAC | CCCCNCNCCC | 900 |
| NAAAYACCCC | MAAAKWTTTCM | AAASMSCNNG | YCCCCC | | | 936 |

(2) INFORMATION FOR SEQ ID NO:336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1042 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| NNNGNKNNNY | ATMMAYTCWY | YCTSCACCSG | GGNNWCWATT | GCGGCCRMW | KCTTGTMAS | 60 |
| AGATCTMNAA | YTCGGCACAG | ASSSGCACAG | ASCCGCGGCG | CTATYCMYCC | GYTGCTCATG | 120 |
| CTCAACACGC | TCKTCGGCGW | GRATAATGGC | NCGCCGCCGG | CGCCAACACG | YTCAAYTGCT | 180 |
| TCGCCAACGC | CATATNTCAA | CAAGGTRATA | AAASCAAAAC | CGCSCGCCGY | GCCCTTGGGC | 240 |
| SCGGRAASCG | GTGCCAACCC | RAAACNCKTT | GGGCACYCGG | KTSRACTTTA | AASGGTAATC | 300 |
| TCKTCCTCCT | GGGCTATGGT | GCGCCACAAA | CCTSYTGCGG | WGGGTCTGGC | CCTGGGYCAC | 360 |
| CGYCRNNTT | TATNTNTCCK | YCTACACNCT | TKGGTYCAAC | CAACCCACTT | CACMAAATTG | 420 |
| TTTTGGGKTG | GGGSSGCCGG | YTGTNNCCGK | TAATAATCSG | NTGKTCSGCC | MYCACCGGWA | 480 |
| CCATANCCTG | GCCGGCCTG | GCAAATTTCC | SAAATCATYT | CCTTCTGRAC | CCCCACAMRC | 540 |
| CTNSAAATCC | GRATCAATNC | CCCNKGGCTT | NTCYCTCTCN | GTRCCCAATY | TGGTTTCTAT | 600 |
| RKTNCCCYAA | TSCAATTGGS | TTYCCRTTSC | YGSTTCCAAN | TTNACAAMAS | GGTTTTYTCM | 660 |
| ACCAAAACCC | NTGGSCCNNA | CMNAAAANKA | RAAAANAKGG | KCTTTYAAAC | CCCCCCTAT | 720 |
| TCAWYCGGTN | CMRNWCCCCG | NGKAAGGKGN | GAAAYTTTHA | CCCAANCCMT | ARSTTSGNAK | 780 |
| AAACCCYYCG | GGGTSMCAAA | MKNWTWTSSC | CTTCGGMCTT | YCCAAATMSA | AAATYYTCKK | 840 |
| KRMNAAAAMC | YGNCCCCSAA | ANATTTTTGT | NAAMCCCKMA | YYTRTTWMCC | WTTTTCCYCC | 900 |
| CCMCNNSNSG | GNTNCCCTTY | TYATTTCYMM | MCRNNSGACN | CCCCMNTYTT | TWTTCKWCN | 960 |
| MMARGSNNYT | RGRMMNMNCC | CCNCCCCNAK | MTCCNCAAAK | NTTTNAACNN | NNKYCKCCCC | 1020 |
| CCCMWNNKNC | CCCCMNCMTT | TM | | | | 1042 |

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

| | | | | | | |
|------------|-------------|------------|------------|-------------|------------|------|
| NNSGSGMKKK | ATAMATCWCT | CTSYACCSNG | GMTCWATTGC | GGCCGMAWTC | TNGTMAASAG | 60 |
| ATCTCGAAYT | CGGCAAAANAK | ACGCMAYGTC | AAGTGTRAYY | CGGTACACATA | TCMTCGCGNG | 120 |
| TCAACMCCAA | AGCCGNGTCA | CCGYCTCCCT | GGGGCGCCAC | CCCCATCGGT | RATGCAACYT | 180 |
| CGCGCGCCAC | CGYCAAAAGG | KTCWTTRAGG | CGCTAAAGGT | CAMCAATTCC | TRAGGTMCN | 240 |
| CACCGTTNTT | TGGCCCGCCC | RAWTYCTRAC | CCGCAATWTC | GGTAATCGGR | AATTTGGGCW | 300 |
| YCGGCTTGGG | CAATAAGKTN | TTGGGCAACG | GCGGRWTCYC | NCTGGCCGRA | ATTCCCNCA | 360 |
| TCCKTTAACG | GKTGRACCGT | TTYCCCGGYT | GCCGTAAYTG | YTYCNTGGGC | GCCYTCGGCC | 420 |
| CRNAGCASY | CRCTAACGGY | CMCCAGGCAA | TACCKTTGGC | TTTRAACCAC | CGGRATNAAY | 480 |
| TGKTACCCAC | YTCAASSGTS | CTGRANTTRK | TNTCNTGRAA | AANMCCACCN | AACCCGGNTT | 540 |
| RATCTGCTTC | MTCANCWTTT | SCCGGGTTCT | GCCGTTTTGR | AAYCTTNATC | CMTYCAAAAG | 600 |
| GTTTAMTTTC | CCAANRAATT | CGGYTTGCCA | CCTTGGCCGS | GGCTGGTTTM | CGMWCCPTRR | 660 |
| AMATCCNCCS | GCGGGSAAAN | AMTTSGGNTT | SGSCCGGTCC | CCCGNAATAT | YCNTGGNCCT | 720 |
| GNAAATTGSS | GGGATCCCCN | GSGNAYCCGG | CCWTKGGGK | TNCCCAGTTG | GWACAATTYC | 780 |
| WKCCGTTCCA | AACCCGGGNC | CGGGGGGTGG | GSCCCNTTTT | CCTMYNNAAA | AAGKGTTTGN | 840 |
| NYTTTTCCTG | CNRAANTTCA | CCSKCNKTNT | GGNCCNAACY | YYYCAANTTC | CANACCTTTA | 900 |
| AASAAANCYK | YGKTYCCCC | TTTTMCCSGS | SANCCCCCM | NMSSKNCGGG | AAAAAAGNK | 960 |
| TYNGCCTTAN | CNSNKTKT | TNKTCCCC | NMWNNSNM | NCBKKCNKRY | NGNSNMNCCT | 1020 |
| MKYSKCNNNN | SNNNNNKC | GSNCSGMKYM | CMNNCNGMYK | NGNKSNNCCC | MSC | 1073 |

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GNSNGNKNTN | TMCAICWYCT | SCACSGGGTC | TATTGCGGCC | GCAATYTNGT | CKASAGATCT | 60 |
| CGATYTCGGC | AMNANAARTG | TCGTCTGCAA | TTTCAGKKTG | GTCKTCAAAY | GGGCCAGGCC | 120 |
| GNGACCRACA | CCCTGNGTCA | CCCAAAANAC | CAACAGCWTC | AAATWTCAAG | GCCRAGGCSC | 180 |
| TRTCAATYCC | CRASCAKTTA | ACCGTKTCCW | TCRAAGGTGC | CRAACCAGGC | ACCCAGYTCA | 240 |
| CCGCCSGGCA | AWTCGCGCTG | CCGGCCGGTN | TCAGCCTGAT | TYCTGACCCT | RWTCTGTSGG | 300 |
| TGGYCAMCNT | GGTGAAGGCC | CWWCCGCCNA | AGAACTGGAG | GGCRAATTCC | CAGGANCCNA | 360 |
| GRAACCCNAG | GAACCCGCGG | TAKAANCCGG | CRAAACCRAG | GCCGYTGCCN | ATTCCNATTA | 420 |
| NAMSGGTTTG | CRACNTGGCC | RAACCGTTTY | CTTGGTCGGC | CTCGGCAACC | CTGGACCANT | 480 |
| TACCCCKTNC | CCGNNMCMAC | CYCGGGTNC | TGKYCCCAAT | NTGCYCCCGC | GNRANTNGGC | 540 |
| CNAATTCCAG | GGCNCCANCT | TTCCGGCCCN | AATTCCTG | GTTAATCACC | GGGCNCNCCT | 600 |
| GTTTGTGGGC | AACCCCN | CCTMTTTTAA | CATTCCGSCC | CAAATGGGNC | STTGGSAAAT | 660 |

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|------|
| TCTNTYCGGT | GGGGCSGGCR | ANMYTTCTCT | YCCNAASAN | CTTAMYCCAN | TTCGSSNTCC | 720 |
| CGGKCAAWS | NGGGGGGNA | AAGGGCCCC | CGGNTSCKCC | GGGGKKGCCC | CYGGKTTCAA | 780 |
| AANTTTCSGG | GKTSTMSCGG | NVTCSCCCCC | CSGCCAAGRA | CCGNGGTTTT | TTTTTGAACC | 840 |
| KCMANTCSSA | AMCCGCCSSC | CCCMAAAGGS | GCCTNAAWGR | RAYTTNKSCC | CNNAAACSGG | 900 |
| CCCCAKYTY | SGGKTTCNNC | CNCCSGKKGT | CCMTSTTTMM | MRCCCTTTGN | GNKTTTTTTAN | 960 |
| MGSCCTTNNC | CACCCCYCK | GGGKCSMNNA | GAAKTMYWKC | CNGGGGNNAN | RSCCCCCCNC | 1020 |
| GSKGGGGKG | MGAGYSCCKT | CTKGCGNCNN | YKNTTTCGCC | C | | 1061 |

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 986 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GNNGNNNKWN | ATMCAYCWYY | CTSCACCSGG | GMTCWATTGC | GGCCGCAWKY | TNGTMAASAG | 60 |
| ATCTMGAAYT | CGGCACANAG | CGGCACAGAG | TGTGTGCATC | TGTGTCANAG | CTGTCAACGC | 120 |
| GGTGCCGCSG | GTGGTRASCA | CMCATTGCGR | AACACCAAAC | CCGTCCGCGG | GYCACCGGCK | 180 |
| TCGCCTGCAA | AAYCCTCCAG | GCCACCYCRA | AACAAWYCT | CCTGCAACSC | ARSCCGTTYC | 240 |
| GCGGCCGRAT | CCTGGKYCAS | YTCGCCKTGC | GGTGCGCCAA | GGTACTGGCS | CWYCRANACC | 300 |
| GCTYCGGGRA | ACCNAACGTA | AATCTTGCCN | AATTTGCNTT | CCCCCTSCCC | TTRATNAATT | 360 |
| TGTTAAACCA | CGCAAACCTY | CGGGCKTCTC | CTCKTGCCRA | WTCCGRWTCC | RATNYCGCCA | 420 |
| TGGCCTNKTC | KYCTYCKYCS | GTMCCCAAAT | CTTGGTATCC | TATATTGTCC | CTAAATGCAA | 480 |
| ATCTKGGCTG | TCCATNTGCT | GGCGTTCAA | TTWAMANCAG | NGGTTTCTTY | CTTCCNAAAC | 540 |
| CCSTTGGCCC | CAAACCNAAA | AATGATNATA | ATAATGGTGC | TNTCAAACCC | CGCNCCTATY | 600 |
| CNATCSGKCC | AMMCCCCRGN | GGKTANKKGG | GNAATTCTMM | AACCCCAAGC | CATAASNTTG | 660 |
| SGANAAACCY | NCNCMGGYCA | CCAAAACANY | NTTNTTGGNY | SSNTTCGGMN | YCATGGCTNN | 720 |
| CMAAAACCCA | AATACTNYYG | GGYCCAATAA | AAMMSGGYC | SAMCCGAAA | WTTTTYTTGN | 780 |
| KYNAAACCN | AAKCTTTTTT | CNAACCCDAN | WNTYCTTNCC | RRCMANTGG | CNSGGARTKT | 840 |
| SSSCTTNCCA | ATGKYCCMAA | AGNGGGRANA | CCARCCCAA | TTCTNNNTIN | KNKNCCCNST | 900 |
| TRNAAAAGGG | GKNTYNMAA | AASCNCCNCC | NCNCTCCCAA | AAKAMCCCN | AAAGAKNTCN | 960 |
| NAANASKYSN | NNNSCCCCC | CCMMMN | | | | 986 |

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| NGNGGGNKRN | ATMMAYCWCT | SATYYACCSN | GGMNMWATTG | CGGCCRMATW | CTNGTMKASA | 60 |
| GATCTMGAAY | YTCGGCAAAG | AGYATKCTCG | GGGGCCAGAT | TTNTGGCCCC | CAACCGCCGC | 120 |
| ACTTTGCAYW | TCAACAKTCC | SGGTGCCCCA | AAAAAWTCWT | ACCCCATMC | TYCKTGCSAM | 180 |
| ASYTGCGCCC | RATTRAACAC | CCGGCCGGCW | TGCTGCGCCA | GGTATTYCAS | CAGYTCAAAY | 240 |
| YCTTTKTAGK | TAAAATCCAG | CSGGCCGGCA | CNCAGCCGGG | CGGKTAGGT | GCCTYCRTCA | 300 |

| | | | | | | |
|------------|------------|-------------|-------------|-------------|-------------|------|
| ATMACCAGCY | CGCCCAGGGY | CACCTTGCCC | AAAAYCTCCT | GGGTCAGCCA | AATTYCCGCS | 360 |
| CCGGCCAACM | ACCANCCGCA | TYCTGGCNTC | AATCYCACCG | GGCCCGGTGY | TAAAMMANMA | 420 |
| GRATCTCKTC | MANCCCCCAN | TCAGCSYTNA | CNGCMACAGC | CCGCCTTCTT | CAMACCGCCA | 480 |
| RTACCGGGWT | CAACCGGCCS | GTCAAACCTCA | ACAGGCGGNC | AGGCCTCCCC | CGGANSAAAG | 540 |
| GTCTTACSCC | NNYAANAAAA | MAAGNTCTGT | TTTCCCCCTC | CASAASNAAA | AANCCCCSGC | 600 |
| CGGGCCTTCN | NMMGGGTTTG | GGGMANANAA | AARCNC CGGN | GGAACGNATC | CGAAAMCTCC | 660 |
| CAAGTCNCMT | TWAWAACYCN | NNAACCCCCC | ANTTTTGGGA | AAGGNTCCCC | NTTMYCCCCC | 720 |
| TTTTASGKTS | GGGMMYYCTY | TAAAAAAATT | CCCCAAAAAG | CCCCGGGAAG | GGTCMAMCTG | 780 |
| GGNAAATTTT | CAAMCCNWGK | TTNTTYNGGT | TMCGGGGGRA | AATTYCNCCTC | CCYYNNNGGG | 840 |
| CSSGSNNNAT | TAYGMSNMT | TTTNNAAWTM | NSGKKTSAAM | YNNKCCMNNN | SNNMSMANNK | 900 |
| TNAMCKCCCN | CCTCNGNGKY | CSCYNCCCSG | GNAGNGGRAS | MKCCNANMAA | AYASGNTTNK | 960 |
| CGGAAMMCNN | AATKGNNNSC | CCGGASMCMN | NNNMAAATMT | CNCNKCNSNN | AANRGMRAACN | 1020 |
| CCCNSNSGMN | RRGAARMTNY | YCCCCCGSKM | GKGNKAAAAW | GKYCCCCCCM | AAAG | 1074 |

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

| | | | | | | |
|-------------|------------|-------------|------------|-------------|------------|------|
| NGNGNCNKNT | MTACATCWTT | CTGCACCSGG | GNTCWANTGC | GGCCGCAWKY | TTGTGASAG | 60 |
| ATCTCGAAYT | CGGCAMGAGG | ACWCTCGCRA | CGCCCCACA | NACTCTGGCG | TGTGTACCCC | 120 |
| ATTGNGCGCK | TCACGCGCCC | AYTGANCCAK | TNCACTGGGG | TGCCGTYCGC | CKTGCGCGGC | 180 |
| GGCCTCACGG | CKCTSCWTCT | RAAGGCWTGG | CGCACCGCAT | TCGGTTTCT | RAACGCTGGG | 240 |
| AAAWTGGCCA | GCCGTCTGGC | TCATGGGNTC | TACGCAACGC | CNGCCCCCAA | CRCTTTCTTA | 300 |
| AATCCGGYCC | NTCCTGANCS | CTTTGAAYCC | CGGGGSAAGA | ACTGGTTGCS | CNCGAYCTGC | 360 |
| TCGAACCTTRK | TCNAAATCCC | GCANAKTGTT | TCNTAMGYCC | CNCCGGAAGG | NGAACCTACT | 420 |
| TTCNGGWANG | TCGGCNKCCG | GCGCTTATCA | STCCTGATCA | ACGGGGAAC | GGYKNNSTTG | 480 |
| KGGGAAAAAG | RRCTCAATG | MTYGGTCCKC | GCTGCGKANC | CGCSCCCTGK | GYCGCNAATG | 540 |
| GAAGGCSMAG | GGTTAANGCC | MTTYCNYCCR | RSCCGTSTGA | SGKWTTYCGG | MGGANKAMNN | 600 |
| NNKMAMWTTK | TCRGNGGCCW | ATSTSCCGGG | CKSTTAKAGA | ANACTYCCKW | WCCGTNTYSC | 660 |
| SAAAGNTKCS | GCGMGTTTTS | SCCKMGANGN | YCTGATTTSA | GGGGGKYKCC | CCCGGGGTYC | 720 |
| CGAAWKWRKY | CCYAGGGGGM | GNYCSAGCSC | CGMNATNAG | AGNAAGGKTT | RYGSTSKNCC | 780 |
| TYTNKGGACC | WSCNNCWSAK | ANAAACNNKKT | TGCSCCNTMS | AGNKTNKGRT | YCCNKTSTTC | 840 |
| TAAGAGGAGC | TATKMKCGCC | CKTGGANGMM | GAGWGMGCGC | KYCCCSNKRT | TCNTNGWAAA | 900 |
| TATKSAGMGG | TKCCGMAGMK | CCSCGTTTCT | TKTGANAAMN | MSMRKNKKTG | CGMGYTCTSC | 960 |
| GGGNTTTGTA | GAGTAKTCGS | CSCSSMWGAC | WCSGCMCGNG | AGKNKTNNNTS | YANTGARCGY | 1020 |
| MNNSKTMKMT | MSCSCGCGNA | GGAGNGCCCC | CSANGMSTGY | NKGGNMSSNG | ARAKGATGGS | 1080 |
| GGCCNCGMNN | MGMGGANMGA | SANNGMGGMR | GGGGGKTGKC | TCKCSCCGNS | CSANGRAGAA | 1140 |
| GKTCNGSCGC | CGMGGKYGKT | KTKTKNKTGG | YSTCMSSMMM | NAGAAAAGAG | AGGGC | 1195 |

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| CCATCTGATC | GTTGGCAACC | AGCATCGCAG | TGGGAACGAT | GCCCTCATTC | AGCATTTGCA | 60 |
| TGGTTTGTG | AAAACCGGAC | ATGGCACTCC | AGTCGCCTTC | CCGTTCCGCT | ATCGGCTGAA | 120 |
| TTTGATTGCG | AGTGAGATAT | TTATGCCAGC | CAGCCAGACG | CAGACGCGCC | GAGACAGAAC | 180 |
| TTAATGGGCC | CGCTAACAGC | GCGATTTGCT | GGTGACCCAA | TGCGACCAGA | TGCTCCACGC | 240 |
| CCAGTCGCGT | ACCGTCTTCA | TGGGAGAAAA | TAATACTGTT | GATGGGTGTC | TGGTCAGAGA | 300 |
| CATCAAGAAA | TAACGCCGGA | ACATTAGTGC | AGGCAGCTTC | CACAGCAATG | GCATCCTGGT | 360 |
| CATCCAGCGG | ATAGTTAATG | ATCAGCCCAC | TGACGCGTTG | CGCGAGAAGA | TTGTGCACCG | 420 |
| CCGCTTTACA | GGCTTCGACG | CCGCTTCGTT | CTACCATCGA | CACCACCACG | CTGGCACCCA | 480 |
| GTTGATCGGC | GCGAGATTTA | ATCGCCGCGA | CAATTTGCGA | CGGCGCGTGC | AGGGCCAGAC | 540 |
| TGGAGGTGGC | AACGCCAATC | AGCAACGACT | GTTTGCCCCG | CAGTTGTTGT | GCCACGCGGT | 600 |
| TGGGAATGTA | ATTGAGCTCC | GCCATCGCCG | CTTCCACTTT | TTCCCGCGTT | TTGCGAGAAA | 660 |
| CGTGGCTGGC | CTGGTTCACC | ACGCGGGAAA | CGGTCTGATA | AGAGACACCG | GCATACTCTG | 720 |
| CGACATCGTA | TAACGTTACT | GGTTTCACAT | TCACCACCCT | GAATTGACTC | TCTTCCGGGC | 780 |
| GCTATCATGC | CATACCGCGA | AAGGTTTTGC | GCCATTCGAT | GGTGTCCGGG | ATCTCGACGC | 840 |
| TCTCCCTTAT | GCGACTCCTG | CATTAGGAAG | CAGCCCAGTA | GTAGGTTGAG | GCCGTTGAGC | 900 |
| ACCGCCGCGG | CAAGGAATGG | TGCATGCAAG | GAGATGGCGC | CCAACAGTCC | CCCGGCCACG | 960 |
| GGGCCTGCCA | CCATACCCAC | GCCGAAACAA | GCGCTCATGA | GCCCGAAGTG | GCGAGCCCGA | 1020 |
| TCTTCCCCAT | CGGTGATGTC | GGCGATATAG | GCGCCAGCAA | CCGCACCTGT | GGCGCCGGTG | 1080 |
| ATGCCGGCCA | CGATGCGTCC | GGCGTAGAGG | ATCGAGATCT | CGATCCCGCG | AAATTAATAC | 1140 |
| GACTCACTAT | AGGGGAATTG | TGAGCGGATA | ACAATTCCCC | TCTAGAAATA | ATTTTGTTTA | 1200 |
| ACTTTAAGAA | GGAGATATAC | ATATGGGCCA | TCATCATCAT | CATCACGTGA | TCGACATCAT | 1260 |
| CGGGACCAGC | CCCACATCCT | GGGAACAGGC | GGCGGCGGAG | GCGGTCCAGC | GGGCGCGGGA | 1320 |
| TAGCGTCGAT | GACATCCGCG | TCGCTCGGGT | CATTGAGCAG | GACATGGCCG | TGGACAGCGC | 1380 |
| CGGCAAGATC | ACCTACCGCA | TCAAGCTCGA | AGTGTCGTTT | AAGATGAGGC | CGGCGCAACC | 1440 |
| GAGGGGCTCG | AAACCACCGA | GCGGTTCGCC | TGAAACGGGC | GCCGGCGCCG | GTACTGTGCG | 1500 |
| GACTACCCCC | GCGTCGTCGC | CGGTGACGTT | GGCGGAGACC | GGTAGCACGC | TGCTCTACCC | 1560 |
| GCTGTTCAAC | CTGTGGGGTC | CGGCCTTTCA | CGAGAGGTAT | CCGAACGTCA | CGATCACCGC | 1620 |
| TCAGGGCACC | GGTTCCTGGT | CCGGGATCGC | GCAGGCCGCC | GCCGGGACGG | TCAACATTGG | 1680 |
| GGCCTCCGAG | GCCTATCTGT | CGGAAGGTGA | TATGGCCGCG | CACAAGGGGC | TGATGAACAT | 1740 |
| CGCGCTAGCC | ATCTCCGCTC | AGCAAGTCAA | CTACAACCTG | CCCGGAGTGA | GCGAGCACCT | 1800 |
| CAAGCTGAAC | GGAAAAGTCC | TGGCGGCCAT | GTACCAGGGC | ACCATCAAAA | CCTGGGACGA | 1860 |
| CCCGCAGATC | GCTGCGCTCA | ACCCCGGCGT | GAACCTGCCC | GGCACCGCGG | TAGTTCCGCT | 1920 |
| GCACCGCTCC | GACGGGTCCG | GTGACACCTT | CTTGTTTACC | CAGTACCTGT | CCAAGCAAGA | 1980 |
| TCCCCAGGGC | TGGGGCAAGT | CGCCCGGCTT | CGGCACCACC | GTCGACTTCC | CGGCGGTGCC | 2040 |
| GGGTGCGCTG | GGTGAGAACG | GCAACGGCGG | CATGGTGACC | GGTTGCGCCG | AGACACCGGG | 2100 |
| CTGCGTGGCC | TATATCGGCA | TCAGCTTCCT | CGACCAGGCC | AGTCAACGGG | GACTCGGCGA | 2160 |
| GGCCCAACTA | GGCAATAGCT | CTGGCAATTT | CTTGTTGCCC | GACGCGCAAA | GCATTCAGGC | 2220 |
| CGCGGCGGCT | GGCTTCGCAT | CGAAAACCCC | GGCGAACCAG | GCGATTTCTG | TGATCGACGG | 2280 |
| GCCCGCCCCG | GACGGCTACC | CGATCATCAA | CTACGAGTAC | GCCATCGTCA | ACAACCGGCA | 2340 |
| AAAGGACGCC | GCCACCGCGC | AGACCTTGCA | GGCATTCTCT | CACTGGGCGA | TCACCGACGG | 2400 |
| CAACAAGGCC | TCGTTCCCTG | ACCAGGTTCA | TTTCCAGCCG | CTGCCGCCCG | CGGTGGTGAA | 2460 |
| GTTGTCTGAC | GCGTTGATCG | CGACGATTTT | CAGCGCTGAG | ATGAAGACCG | ATGCCGCTAC | 2520 |
| CCTCGCGCAG | GAGGCAGGTA | ATTTGAGCGG | GATCTCCGGC | GACCTGAAAA | CCGAGATCGA | 2580 |
| CCAGGTGGAG | TCGACGGCAG | GTTGCTTGCA | GGGCCAGTGG | CGCGGCGCGG | CGGGGACGGC | 2640 |
| CGCCACAGCC | GCGGTGGTGC | GCTTCCAAGA | AGCAGCAAT | AAGCAGAAGC | AGGAACTCGA | 2700 |
| CGAGATCTCG | ACGAATATTC | GTCAGGCCGG | CGTCCAATAC | TCGAGGGCCG | ACGAGGAGCA | 2760 |
| GCAGCAGGCG | CTGTCTCTCG | AAATGGGCTT | TGGATTGAGC | TTGCGGCTGC | CTGCTGGCTG | 2820 |
| GGTGGAGTCT | GACGCCGCCC | ACTTCGACTA | CGGTTCAGCA | CTCCTCAGCA | AAACCACCGG | 2880 |
| GGACCCGCCA | TTTCCCGGAC | AGCCGCCGCC | GGTGGCCAAT | GACACCCGTA | TCGTGCTCGG | 2940 |
| CCGGCTAGAC | CAAAAGCTTT | ACGCCAGCGC | CGAAGCCACC | GACTCCAAGG | CCGCGGCCCG | 3000 |
| GTTGGGCTCG | GACATGGGTG | AGTTCTATAT | GCCCTACCCG | GGCACCCGGA | TCAACCAGGA | 3060 |

AACCGTCTCG CTYGACGCCA ACGGGGTGTC TGGAAGCGCG TCGTATTACG AAGTCAAGTT 3120
 CAGCGATCCG AGTAAGCCGA ACGGCCAGAT CTGGACGGGC GTAATCGGCT CGCCCGCGGC 3180
 GAACGCACCG GACGCCGGGC CCCCTCAGCG CTGGTTTGTG GTATGGCTCG GGACCGCCAA 3240
 CAACCCGGTG GACAAGGGCG CGGCCAAGGC GCTGGCCGAA TCGATCCGCG CTTTGGTTCG 3300
 CCCGCCGCCG GCGCCGGCCG GGGAAAGTCG TCCTACCCCG ACGACACCGA CACCGCAGCG 3360
 GACCTTACCG GCCTGAGAAT TCTGCAGATA TCCATCACAC TGGCGGCCGC TCGAGCACCA 3420
 CCACCACCAC CACTGAGATC CGGCTGCTAA CAAAGCCCGA AAGGAAGCTG AGTTGGCTGC 3480
 TGCCACCGCT GAGCAATAAC TAGCATAACC CCTTGGGGCC TCTAAACGGG TCTTGAGGGG 3540
 TTTTGTGCTG AAAGGAGGAA CTATATCCGG AT 3572

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Gln | Phe | Gln | Ser | Gly | Gly | Asp | Asn | Ser | Pro | Ala | Val | Tyr | Xaa | Xaa |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Asp | Gly | Xaa | Arg | | | | | | | | | | | | |
| | | | 20 | | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

| | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Thr | Val | Pro | Xaa | Val | Thr | Glu | Ala | Arg |
| 1 | | | | 5 | | | | | 10 |

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

| | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Thr | Pro | Ser | Xaa | Val | Ala | Phe | Ala | Arg |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

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10

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Asp Ala Gly Lys Xaa Ala Gly Xaa Asp Val Xaa Arg
 1 5 10

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Thr Xaa Glu Glu Xaa Gln Glu Ser Phe Asn Ser Ala Ala Pro Gly Asn
 1 5 10 15
 Xaa Lys

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

CTAGTTAGTA CTCAGTCGCA GACCGTG

27

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

GCAGTGACGA ATTCACTTCG ACTCC

25

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|------|
| CATATGGGCC | ATCATCATCA | TCATCACGTG | ATCGACATCA | TCGGGACCAG | CCCCACATCC | 60 |
| TGGGAACAGG | CGGCGGCGGA | GGCGGTCCAG | CGGGCGCGGG | ATAGCGTCGA | TGACATCCGC | 120 |
| GTCGCTCGGG | TCATTGAGCA | GGACATGGCC | GTGGACAGCG | CCGGCAAGAT | CACCTACCGC | 180 |
| ATCAAGCTCG | AAGTGTCTGT | CAAGATGAGG | CCGGCGCAAC | CGAGGGGCTC | GAAACCACCG | 240 |
| AGCGGTTTCG | CTGAAACGGG | CGCCGGCGCC | GGTACTGTCT | CGACTACCCC | CGCGTCGTCG | 300 |
| CCGGTGACGT | TGGCGGAGAC | CGGTAGCACG | CTGCTCTACC | CGCTGTTCAA | CCTGTGGGGT | 360 |
| CCGGCCTTTC | ACGAGAGGTA | TCCGAACGTC | ACGATCACCG | CTCAGGGCAC | CGGTTCTGGT | 420 |
| GCCGGGATCG | CGCAGGCCGC | CGCCGGGACG | GTCAACATTG | GGGCCTCCGA | CGCCTATCTG | 480 |
| TCGGAAGGTG | ATATGGCCGC | GCACAAGGGG | CTGATGAACA | TCGCGCTAGC | CATCTCCGCT | 540 |
| CAGCAGGTCA | ACTACAACCT | GCCCCGAGTG | AGCGAGCACC | TCAAGCTGAA | CGGAAAAGTC | 600 |
| CTGGCGGCCA | TGTACCAGGG | CACCATCAAA | ACCTGGGACG | ACCCGCAGAT | CGCTGCGCTC | 660 |
| AACCCCGCGC | TGAACCTGCC | CGGCACCGCG | GTAGTTCCGC | TGCACCGCTC | CGACGGGTCC | 720 |
| GGTGACACCT | TCTTGTTTAC | CCAGTACCTG | TCCAAGCAAG | ATCCCGAGGG | CTGGGGCAAG | 780 |
| TCGCCCCGCT | TCGGCACCAC | CGTCGACTTC | CCGGCGGTGC | CGGGTGCCTG | GGGTGAGAAC | 840 |
| GGCAACGGCG | GCATGGTGAC | CGGTTGCGCC | GAGACACCGG | GCTGCGTGGC | CTATATCGGC | 900 |
| ATCAGCTTCC | TCGACCAGGC | CAGTCAACGG | GGACTCGGCG | AGGCCCAACT | AGGCAATAGC | 960 |
| TCTGGCAATT | TCTTGTTGCC | CGACGCGCAA | AGCATTCAGG | CCGCGGCGGC | TGGCTTCGCA | 1020 |
| TCGAAAACCT | CGCGGAACCA | GGCGATTTTC | ATGATCGACG | GGCCCGCCCC | GGACGGCTAC | 1080 |
| CCGATCATCA | ACTAGAGTA | CGCCATCGTC | AACAACCGGC | AAAAGGACGC | CGCCACCGCG | 1140 |
| CAGACCTTGC | AGGCATTTCT | GCACTGGGCG | ATCACCGACG | GCAACAAGGC | CTCGTTCTCT | 1200 |
| GACCAGGTTT | ATTTCAGGCC | GCTGCCGCCC | GCGGTGGTGA | AGTTGTCTGA | CGCGTTGATC | 1260 |
| GCGACGATTT | CCAGCGCTGA | GATGAAGACC | GATGCCGCTA | CCCTCGCGCA | GGAGGCAGGT | 1320 |
| AATTTTCGAG | GGATCTCCGG | CGACCTGAAA | ACCCAGATCG | ACCAGGTGGA | GTCGACGGCA | 1380 |
| GGTTTCGTTG | AGGGCCAGTG | GCGCGGCGCG | GCGGGGACGG | CCGCCCAGGC | CGCGGTGGTG | 1440 |
| CGCTTCCAAG | AAGCAGCCAA | TAAGCAGAAG | CAGGAACCTG | ACGAGATCTC | GACGAATATT | 1500 |
| CGTCAGGCCG | GCGTCCAATA | CTCGAGGGCC | GACGAGGAGC | AGCAGCAGGC | GCTGTCTCTG | 1560 |
| CAAATGGGCT | TTGTGCCAC | AACGGCCGCC | TCGCCGCCGT | CGACCGCTGC | AGCGCCACCC | 1620 |
| GCACCGGCGA | CACCTGTTGC | CCCCCCACCA | CCGGCCGCCG | CCAACACGCC | GAATGCCAG | 1680 |
| CCGGGCGATC | CCAACGCAGC | ACCTCCGCCG | GCCGACCCGA | ACGCACCGCC | GCCACCTGTC | 1740 |
| ATTGCCCAA | ACGCACCCCA | ACCTGTCCGG | ATCGACAACC | CGGTTGGAGG | ATTGAGCTTC | 1800 |
| GCGCTGCCTG | CTGGCTGGGT | GGAGTCTGAC | GCCGCCCACT | TCGACTACGG | TTCAGCACTC | 1860 |
| CTCAGCAAAA | CCACCGGGGA | CCCGCCATTT | CCCGGACAGC | CGCCGCCGGT | GGCCAAATGAC | 1920 |
| ACCCGTATCG | TGCTCGGCCG | GCTAGACCAA | AAGCTTTACG | CCAGCGCCGA | AGCCACCGAC | 1980 |
| TCCAAGGCCG | CGGCCCGGTT | GGGCTCGGAC | ATGGGTGAGT | TCTATATGCC | CTACCCGGGC | 2040 |
| ACCCGGATCA | ACCAGGAAAC | CGTCTCGCTC | GACGCCAACG | GGGTGTCTGG | AAGCGCGTCG | 2100 |
| TATTACGAAG | TCAAGTTCAG | CGATCCGAGT | AAGCCGAACG | GCCAGATCTG | GACGGGCGTA | 2160 |

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ATCGGCTCGC CCGCGGCGAA CGCACCGGAC GCCGGGGCCCC CTCAGCGCTG GTTTGTGGTA 2220
TGGCTCGGGA CCGCCAACAA CCCGGTGGAC AAGGGCGCGG CCAAGGCGCT GGCCGAATCG 2280
ATCCGGCCTT TGGTCGCCCC GCCGCCGGCG CCGGCACCGG CTCCTGCAGA GCGCGCTCCG 2340
GCGCCGGCGC CGGCCGGGGA AGTCGCTCCT ACCCCGACGA CACCGACACC GCAGCGGACC 2400
TTACCGGCCT GA 2412

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(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

```

Met Gly His His His His His Val Ile Asp Ile Ile Gly Thr Ser
 1           5           10           15
Pro Thr Ser Trp Glu Gln Ala Ala Ala Glu Ala Val Gln Arg Ala Arg
 20           25           30
Asp Ser Val Asp Asp Ile Arg Val Ala Arg Val Ile Glu Gln Asp Met
 35           40           45
Ala Val Asp Ser Ala Gly Lys Ile Thr Tyr Arg Ile Lys Leu Glu Val
 50           55           60
Ser Phe Lys Met Arg Pro Ala Gln Pro Arg Gly Ser Lys Pro Pro Ser
 65           70           75           80
Gly Ser Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro
 85           90           95
Ala Ser Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr
100          105          110
Pro Leu Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn
115          120          125
Val Thr Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln
130          135          140
Ala Ala Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser
145          150          155          160
Glu Gly Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala
165          170          175
Ile Ser Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His
180          185          190
Leu Lys Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile
195          200          205
Lys Thr Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn
210          215          220
Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly
225          230          235          240
Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly
245          250          255
Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val
260          265          270
Pro Gly Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys
275          280          285
Ala Glu Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp

```

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| | | | | |
|---|-----|-----|-----|-----|
| 290 | | 295 | | 300 |
| Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser | | | | |
| 305 | | 310 | | 315 |
| Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala | | | | |
| | 325 | | 330 | 335 |
| Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp | | | | |
| | 340 | | 345 | 350 |
| Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile | | | | |
| | 355 | | 360 | 365 |
| Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala | | | | |
| | 370 | | 375 | 380 |
| Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp | | | | |
| 385 | | 390 | | 395 |
| Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp | | | | |
| | 405 | | 410 | 415 |
| Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala | | | | |
| | 420 | | 425 | 430 |
| Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu | | | | |
| | 435 | | 440 | 445 |
| Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly | | | | |
| | 450 | | 455 | 460 |
| Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg | | | | |
| 465 | | 470 | | 475 |
| Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser | | | | |
| | 485 | | 490 | 495 |
| Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu | | | | |
| | 500 | | 505 | 510 |
| Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala | | | | |
| | 515 | | 520 | 525 |
| Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro | | | | |
| | 530 | | 535 | 540 |
| Val Ala Pro Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro | | | | |
| 545 | | 550 | | 555 |
| Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro | | | | |
| | 565 | | 570 | 575 |
| Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn | | | | |
| | 580 | | 585 | 590 |
| Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser | | | | |
| | 595 | | 600 | 605 |
| Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr | | | | |
| | 610 | | 615 | 620 |
| Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr | | | | |
| 625 | | 630 | | 635 |
| Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu | | | | |
| | 645 | | 650 | 655 |
| Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu | | | | |
| | 660 | | 665 | 670 |
| Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser | | | | |
| | 675 | | 680 | 685 |
| Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys | | | | |
| | 690 | | 695 | 700 |
| Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile | | | | |
| 705 | | 710 | | 715 |
| Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp | | | | |
| | 725 | | 730 | 735 |

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Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala
 740 745 750
 Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro
 755 760 765
 Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala
 770 775 780
 Gly Glu Val Ala Pro Thr Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu
 785 790 795 800
 Pro Ala

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

GGATCCAAAC CACCGAGCGG TTCGCCTGAA ACGG

34

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

CGCTGCGAAT TCACCTCCGG AGGAAATCGT CGCGATC

37

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

| | |
|--|-----|
| CATATGGGCC ATCATCATCA TCATCACGGA TCCAAACCAC CGAGCGGTTC GCCTGAAACG | 60 |
| GGCGCCGGCG CCGGTACTGT CGCGACTACC CCCGCGTCGT CGCCGGTGAC GTTGGCGGAG | 120 |
| ACCGGTAGCA CGCTGCTCTA CCCGCTGTTC AACCTGTGGG GTCCGGCCTT TCACGAGAGG | 180 |
| TATCCGAACG TCACGATCAC CGCTCAGGGC ACCGGTCTCTG GTGCCGGGAT CGCGCAGGCC | 240 |

GCCGCCGGGA CGGTCAACAT TGGGGCCTCC GACGCCTATC TGTCGGAAGG TGATATGGCC 300
 GCGCACAAGG GGCTGATGAA CATCGCGCTA GCCATCTCCG CTCAGCAGGT CAACTACAAC 360
 CTGCCCCGAG TGAGCGAGCA CCTCAAGCTG AACCGAAAAAG TCCTGGCGGC CATGTACCAG 420
 GGCACCATCA AAACCTGGGA CGACCCGCAG ATCGCTGCGC TCAACCCCGG CGTGAACCTG 480
 CCCGGCACCG CGGTAGTTCC GCTGCACCGC TCCGACGGGT CCGGTGACAC CTTCTTGTTT 540
 ACCCAGTACC TGTCCAAGCA AGATCCCAGG GGCTGGGGCA AGTCGCCCGG CTTCCGGCACC 600
 ACCGTCGACT TCCCGGCGGT GCCGGGTGCG CTGGGTGAGA ACGGCAACGG CGGCATGGTG 660
 ACCGGTTGCG CCGAGACACC GGGCTGCGTG GCCTATATCG GCATCAGCTT CCTCGACCAG 720
 GCCAGTCAAC GGGGACTCGG CGAGGCCCAA CTAGGCAATA GCTCTGGCAA TTTCTTGTTG 780
 CCCGACGCGC AAAGCATTCA GGCCGCGGCG GCTGGCTTCG CATCGAAAAAC CCCGGCGAAC 840
 CAGGCGATTT CGATGATCGA CGGGCCCGCC CCGGACGGCT ACCCGATCAT CAACTACGAG 900
 TACGCCATCG TCAACAACCG GCAAAAGGAC GCCGCCACCG CGCAGACCTT GCAGGCATTT 960
 CTGCACTGGG CGATCACCAG CGGCAACAAG GCCTCGTTCC TCGACCAGGT TCATTTCCAG 1020
 CCGCTGCCCG CCGCGGTGGT GAAGTTGTCT GACGCGTTGA TCGCGACGAT TTCCTCCGGA 1080
 GGTGGCAGTG GGGGAGGCTC AGGTGGAGGT TCTGGCGGGA GCGTGCCAC AACGGCCGCC 1140
 TCGCCCGGTG CGACCGCTGC AGCGCCACCG GCACCGGCGA CACCTGTTGC CCCCCACCA 1200
 CCGGCCGCGG CCAACACGCC GAATGCCAG CCGGGCGATC CCAACGCAGC ACCTCCGCGG 1260
 GCCGACCCGA ACGCACCGCC GCCACCTGTC ATTGCCCCAA ACGCACCCCA ACCTGTCCGG 1320
 ATCGACAACC CGGTTGGAGG ATTCAGCTTC GCGCTGCCTG CTGGCTGGGT GGAGTCTGAC 1380
 GCCGCCCACT TCGACTACGG TTCAGCACTC CTCAGCAAAA CCACCGGGGA CCCGCCATTT 1440
 CCCGGACAGC CGCCGCCGGT GGCCAATGAC ACCCGTATCG TGCTCGGCCG GCTAGACCAA 1500
 AAGCTTTACG CCAGCGCCGA AGCCACCGAC TCCAAGGCCG CGGCCCGGTT GGGCTCGGAC 1560
 ATGGGTGAGT TCTATATGCC CTACCCGGGC ACCCGGATCA ACCAGGAAAC CGTCTCGCTC 1620
 GACCCAACG GGGTGTCTGG AAGCGCGTCG TATTACGAAG TCAAGTTCAG CGATCCGAGT 1680
 AAGCCGAACG GCCAGATCTG GACGGGCGTA ATCGGCTCGC CCGCGGCGAA CGCACCGGAC 1740
 GCCGGGCCCC CTCAGCGCTG GTTTGTGGTA TGGCTCGGGA CCGCCAACAA CCCGGTGGAC 1800
 AAGGGCGCGG CCAAGGCGCT GGCCGAATCG ATCCGGCCTT TGGTCGCCCC GCCGCCGGCG 1860
 CCGGCACCGG CTCCTGCAGA GCCCGTCCG GCGCCGGCGC CGGCCGGGGA AGTCGCTCCT 1920
 ACCCCGACGA CACCGACACC GCAGCGGACC TTACCGGCCT GA 1962

(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

Met Gly His His His His His Gly Ser Lys Pro Pro Ser Gly Ser
 1 5 10 15
 Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 20 25 30
 Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 35 40 45
 Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 50 55 60
 Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 65 70 75 80
 Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
 85 90 95
 Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gln | Gln | Val | Asn | Tyr | Asn | Leu | Pro | Gly | Val | Ser | Glu | His | Leu | Lys |
| 115 | | | | | | | | 120 | | | | | 125 | | |
| Leu | Asn | Gly | Lys | Val | Leu | Ala | Ala | Met | Tyr | Gln | Gly | Thr | Ile | Lys | Thr |
| 130 | | | | | | | 135 | | | | | 140 | | | |
| Trp | Asp | Asp | Pro | Gln | Ile | Ala | Ala | Leu | Asn | Pro | Gly | Val | Asn | Leu | Pro |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Gly | Thr | Ala | Val | Val | Pro | Leu | His | Arg | Ser | Asp | Gly | Ser | Gly | Asp | Thr |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Phe | Leu | Phe | Thr | Gln | Tyr | Leu | Ser | Lys | Gln | Asp | Pro | Glu | Gly | Trp | Gly |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Lys | Ser | Pro | Gly | Phe | Gly | Thr | Thr | Val | Asp | Phe | Pro | Ala | Val | Pro | Gly |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Ala | Leu | Gly | Glu | Asn | Gly | Asn | Gly | Gly | Met | Val | Thr | Gly | Cys | Ala | Glu |
| 210 | | | | | | 215 | | | | | | 220 | | | |
| Thr | Pro | Gly | Cys | Val | Ala | Tyr | Ile | Gly | Ile | Ser | Phe | Leu | Asp | Gln | Ala |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Ser | Gln | Arg | Gly | Leu | Gly | Glu | Ala | Gln | Leu | Gly | Asn | Ser | Ser | Gly | Asn |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Phe | Leu | Leu | Pro | Asp | Ala | Gln | Ser | Ile | Gln | Ala | Ala | Ala | Ala | Gly | Phe |
| | | | 260 | | | | | 265 | | | | | | 270 | |
| Ala | Ser | Lys | Thr | Pro | Ala | Asn | Gln | Ala | Ile | Ser | Met | Ile | Asp | Gly | Pro |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Ala | Pro | Asp | Gly | Tyr | Pro | Ile | Ile | Asn | Tyr | Glu | Tyr | Ala | Ile | Val | Asn |
| 290 | | | | | | 295 | | | | | | 300 | | | |
| Asn | Arg | Gln | Lys | Asp | Ala | Ala | Thr | Ala | Gln | Thr | Leu | Gln | Ala | Phe | Leu |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| His | Trp | Ala | Ile | Thr | Asp | Gly | Asn | Lys | Ala | Ser | Phe | Leu | Asp | Gln | Val |
| | | | | 325 | | | | 330 | | | | | | 335 | |
| His | Phe | Gln | Pro | Leu | Pro | Pro | Ala | Val | Val | Lys | Leu | Ser | Asp | Ala | Leu |
| | | | 340 | | | | | 345 | | | | | 350 | | |
| Ile | Ala | Thr | Ile | Ser | Ser | Gly | Gly | Gly | Ser | Gly | Gly | Gly | Ser | Gly | Gly |
| | | 355 | | | | 360 | | | | | | 365 | | | |
| Gly | Ser | Gly | Gly | Ser | Val | Pro | Thr | Thr | Ala | Ala | Ser | Pro | Pro | Ser | Thr |
| 370 | | | | | | 375 | | | | | | 380 | | | |
| Ala | Ala | Ala | Pro | Pro | Ala | Pro | Ala | Thr | Pro | Val | Ala | Pro | Pro | Pro | Pro |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| Ala | Ala | Ala | Asn | Thr | Pro | Asn | Ala | Gln | Pro | Gly | Asp | Pro | Asn | Ala | Ala |
| | | | 405 | | | | | 410 | | | | | 415 | | |
| Pro | Pro | Pro | Ala | Asp | Pro | Asn | Ala | Pro | Pro | Pro | Pro | Val | Ile | Ala | Pro |
| | | | 420 | | | | | 425 | | | | | 430 | | |
| Asn | Ala | Pro | Gln | Pro | Val | Arg | Ile | Asp | Asn | Pro | Val | Gly | Gly | Phe | Ser |
| | | 435 | | | | 440 | | | | | | 445 | | | |
| Phe | Ala | Leu | Pro | Ala | Gly | Trp | Val | Glu | Ser | Asp | Ala | Ala | His | Phe | Asp |
| 450 | | | | | 455 | | | | | | 460 | | | | |
| Tyr | Gly | Ser | Ala | Leu | Leu | Ser | Lys | Thr | Thr | Gly | Asp | Pro | Pro | Phe | Pro |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| Gly | Gln | Pro | Pro | Pro | Val | Ala | Asn | Asp | Thr | Arg | Ile | Val | Leu | Gly | Arg |
| | | | | 485 | | | | 490 | | | | | 495 | | |
| Leu | Asp | Gln | Lys | Leu | Tyr | Ala | Ser | Ala | Glu | Ala | Thr | Asp | Ser | Lys | Ala |
| | | | 500 | | | | | 505 | | | | | 510 | | |
| Ala | Ala | Arg | Leu | Gly | Ser | Asp | Met | Gly | Glu | Phe | Tyr | Met | Pro | Tyr | Pro |
| | | 515 | | | | 520 | | | | | | 525 | | | |
| Gly | Thr | Arg | Ile | Asn | Gln | Glu | Thr | Val | Ser | Leu | Asp | Ala | Asn | Gly | Val |
| 530 | | | | | | 535 | | | | | | 540 | | | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Gly | Ser | Ala | Ser | Tyr | Tyr | Glu | Val | Lys | Phe | Ser | Asp | Pro | Ser | Lys |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 |
| Pro | Asn | Gly | Gln | Ile | Trp | Thr | Gly | Val | Ile | Gly | Ser | Pro | Ala | Ala | Asn |
| | | | | 565 | | | | | 570 | | | | | | 575 |
| Ala | Pro | Asp | Ala | Gly | Pro | Pro | Gln | Arg | Trp | Phe | Val | Val | Trp | Leu | Gly |
| | | | 580 | | | | | 585 | | | | | | 590 | |
| Thr | Ala | Asn | Asn | Pro | Val | Asp | Lys | Gly | Ala | Ala | Lys | Ala | Leu | Ala | Glu |
| | | 595 | | | | | 600 | | | | | 605 | | | |
| Ser | Ile | Arg | Pro | Leu | Val | Ala | Pro | Pro | Pro | Ala | Pro | Ala | Pro | Ala | Pro |
| | 610 | | | | | 615 | | | | | 620 | | | | |
| Ala | Glu | Pro | Ala | Pro | Ala | Pro | Ala | Pro | Ala | Gly | Glu | Val | Ala | Pro | Thr |
| 625 | | | | | 630 | | | | | 635 | | | | | 640 |
| Pro | Thr | Thr | Pro | Thr | Pro | Gln | Arg | Thr | Leu | Pro | Ala | | | | |
| | | | | 645 | | | | | 650 | | | | | | |

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